

SEQUENCE LISTING

<110> BASF Aktiengesellschaft

<120> MetF

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<212> DNA

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<223> RDI01260

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Val	Ile	Ser	Met	Pro	Thr	Pro	Gly	Gln	Val	Pro	Phe	Ser	Val	Glu	Phe	
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Met	Pro	Pro	Arg	Asp	Glu	Ala	Ala	Glu	Glu	Arg	Leu	Trp	Lys	Ala	Ala	
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gaa	gca	ttt	cac	gac	tta	gga	gcc	tct	ttt	gtc	tcc	gtt	act	tat	ggc	192
Glu	Ala	Phe	His	Asp	Leu	Gly	Ala	Ser	Phe	Val	Ser	Val	Thr	Tyr	Gly	
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gca	ggc	gga	tct	agc	cgc	gag	cgc	aca	atg	cgt	gtc	gcg	cac	aag	ctt	240
Ala	Gly	Gly	Ser	Ser	Arg	Glu	Arg	Thr	Met	Arg	Val	Ala	His	Lys	Leu	
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tct	cgt	cat	ccg	ttg	acc	acg	ctc	gtt	cat	ctc	acg	ctt	gtg	gaa	cac	288
Ser	Arg	His	Pro	Leu	Thr	Thr	Leu	Val	His	Leu	Thr	Leu	Val	Glu	His	
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acc	caa	gaa	gaa	tta	gaa	gaa	att	ctg	tgc	act	tat	gcg	tcc	cac	ggg	336
Thr	Gln	Glu	Glu	Leu	Glu	Glu	Ile	Leu	Cys	Thr	Tyr	Ala	Ser	His	Gly	
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Gly	Ile	Ala	Ser	Phe	Pro	Glu	Gly	His	Tyr	Arg	Ala	Pro	Ser	Ile	Glu	
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Ser	Ile	Thr	Gln	Met	Phe	Phe	Asp	Val	Asp	His	Tyr	Leu	Arg	Leu	Arg	
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Asp	Arg	Leu	Val	Lys	Ala	Asp	Pro	Glu	His	Gly	Ser	Lys	Pro	Ile	Ile	
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Pro	Gly	Leu	Met	Pro	Ile	Thr	Ser	Leu	Arg	Ser	Val	Arg	Arg	Gln	Met	
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Glu	Leu	Ala	Gly	Ala	Thr	Leu	Pro	Lys	Ala	Leu	Glu	Lys	Arg	Leu	Leu	
				245					250					255		
gac	gca	gcg	cgc	ggc	gat	gag	gaa	gct	cat	cgc	ggc	gat	att	cgc	aaa	816
Asp	Ala	Ala	Arg	Gly	Asp	Glu	Glu	Ala	His	Arg	Gly	Asp	Ile	Arg	Lys	
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gta	gga	atc	gaa	gtc	act	act	gag	atg	gca	cag	cgt	ctt	att	tct	gaa	864
Val	Gly	Ile	Glu	Val	Thr	Thr	Glu	Met	Ala	Gln	Arg	Leu	Ile	Ser	Glu	
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Gly	Ile	Pro	Asp	Ile	His	Phe	Met	Thr	Met	Asn	Tyr	Val	Arg	Ala	Thr	
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Gln	Glu	Val	Leu	His	Asn	Leu	Gly	Met	Ala	Pro	Ala	Trp	Gly	Thr	Gln	
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<212> PRT

<213> corynebacterium diptheriae

<400> 2

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Gln	Glu	Val	Leu	His	Asn	Leu	Gly	Met	Ala	Pro	Ala	Trp	Gly	Thr	Gln
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<213> Streptomyces lividans

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20 25 30	
gcg ccg aag acg ccc aag ggc gag aag aac ctc tgg agc gcg ctg cgg	144
Ala Pro Lys Thr Pro Lys Gly Glu Lys Asn Leu Trp Ser Ala Leu Arg	
35 40 45	
cgg gtc gag gcc gtg gcc ccg gac ttc gtc tcc gtg acc tac ggc gcc	192
Arg Val Glu Ala Val Ala Pro Asp Phe Val Ser Val Thr Tyr Gly Ala	
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ggc ggc tcc acg cgc gcc ggc acg gtc cgc gag acc cag cag atc gtc	240
Gly Gly Ser Thr Arg Ala Gly Thr Val Arg Glu Thr Gln Gln Ile Val	
65 70 75 80	
gcc gac acc acg ctg acc ccg gtg gcc cac ctc acc gcc gtc gac cac	288
Ala Asp Thr Thr Leu Thr Pro Val Ala His Leu Thr Ala Val Asp His	
85 90 95	
tcc gtc gcc gag ctg cgc aac atc atc ggc cag tac gcc gac gcc ggg	336
Ser Val Ala Glu Leu Arg Asn Ile Ile Gly Gln Tyr Ala Asp Ala Gly	
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atc cgc aac atg ctg gcc gtg cgc ggc gac ccg ccc ggc gac ccg aac	384
Ile Arg Asn Met Leu Ala Val Arg Gly Asp Pro Pro Gly Asp Pro Asn	
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gcc gac tgg atc gcg cac ccc gag ggc ctg acc tac gcg gcc gaa ctg	432
Ala Asp Trp Ile Ala His Pro Glu Gly Leu Thr Tyr Ala Ala Glu Leu	
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gtc agg ctc atc aag gag tcg gga gac ttc tgc gtc ggc gtc gcc gcc	480
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Phe Pro Glu Met His Pro Arg Ser Ala Asp Trp Asp Thr Asp Val Thr	
165 170 175	
aac ttc gtc gac aag tgc cgg gcc ggc gcc gac tac gcc atc acc cag	576
Asn Phe Val Asp Lys Cys Arg Ala Gly Ala Asp Tyr Ala Ile Thr Gln	
180 185 190	
atg ttc ttc cag ccc gac tcc tac ctc cgg ctg cgc gac cgg gtc gcc	624
Met Phe Phe Gln Pro Asp Ser Tyr Leu Arg Leu Arg Asp Arg Val Ala	
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ccg gcg gag ctg aaa gag cgg atc ctc aca gcc aag gac gat ccg gcg			768
Pro Ala Glu Leu Lys Glu Arg Ile Leu Thr Ala Lys Asp Asp Pro Ala			
	245	250	255
gct gta cgc tcg atc ggc atc gag ttc gcc acg gag ttc tgc gcg cgg			816
Ala Val Arg Ser Ile Gly Ile Glu Phe Ala Thr Glu Phe Cys Ala Arg			
	260	265	270
ctg ctg gcc gag gga gtg cca gga ctg cac ttc atc acg ctc aac aac			864
Leu Leu Ala Glu Gly Val Pro Gly Leu His Phe Ile Thr Leu Asn Asn			
	275	280	285
tcc acg gcg acg ctg gaa atc tac gag aac ctg ggc ctg cac cac cca			912
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Pro Arg Ala			
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 35 40 45
 Arg Val Glu Ala Val Ala Pro Asp Phe Val Ser Val Thr Tyr Gly Ala
 50 55 60
 Gly Gly Ser Thr Arg Ala Gly Thr Val Arg Glu Thr Gln Gln Ile Val
 65 70 75 80
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 85 90 95
 Ser Val Ala Glu Leu Arg Asn Ile Ile Gly Gln Tyr Ala Asp Ala Gly
 100 105 110
 Ile Arg Asn Met Leu Ala Val Arg Gly Asp Pro Pro Gly Asp Pro Asn
 115 120 125
 Ala Asp Trp Ile Ala His Pro Glu Gly Leu Thr Tyr Ala Ala Glu Leu
 130 135 140
 Val Arg Leu Ile Lys Glu Ser Gly Asp Phe Cys Val Gly Val Ala Ala

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			180					185					190		
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Ala	Ala	Gly	Cys	Ala	Thr	Pro	Val	Ile	Pro	Glu	Val	Met	Pro	Val	Thr
	210					215					220				
Ser	Val	Lys	Met	Leu	Glu	Arg	Leu	Pro	Lys	Leu	Ser	Asn	Ala	Ser	Phe
225					230					235					240
Pro	Ala	Glu	Leu	Lys	Glu	Arg	Ile	Leu	Thr	Ala	Lys	Asp	Asp	Pro	Ala
				245					250					255	
Ala	Val	Arg	Ser	Ile	Gly	Ile	Glu	Phe	Ala	Thr	Glu	Phe	Cys	Ala	Arg
			260					265					270		
Leu	Leu	Ala	Glu	Gly	Val	Pro	Gly	Leu	His	Phe	Ile	Thr	Leu	Asn	Asn
		275					280					285			
Ser	Thr	Ala	Thr	Leu	Glu	Ile	Tyr	Glu	Asn	Leu	Gly	Leu	His	His	Pro
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 <223> RSX01699

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Arg Asp Ile Leu Ala Thr Gly Lys Thr Thr Tyr Ser Phe Glu Phe Ser	
20 25 30	
gcg ccg aag acg ccc aag ggc gag agg aac ctc tgg agc gcg ctg cgg	144
Ala Pro Lys Thr Pro Lys Gly Glu Arg Asn Leu Trp Ser Ala Leu Arg	
35 40 45	
cgg gtc gag gcc gtg gcc ccg gac ttc gtc tcc gtg acc tac ggc gcc	192
Arg Val Glu Ala Val Ala Pro Asp Phe Val Ser Val Thr Tyr Gly Ala	
50 55 60	
ggc ggc tcc acg cgc gcc ggc acg gtc cgc gag acc cag cag atc gtc	240

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Ala	Asp	Thr	Thr	Leu	Thr	Pro	Val	Ala	His	Leu	Thr	Ala	Val	Asp	His	
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tcc	gtc	gcc	gag	ctg	cgc	aac	atc	atc	ggc	cag	tac	gcc	gac	gcc	ggg	336
Ser	Val	Ala	Glu	Leu	Arg	Asn	Ile	Ile	Gly	Gln	Tyr	Ala	Asp	Ala	Gly	
			100					105					110			
atc	cgc	aac	atg	ctg	gcc	gtg	cgc	ggc	gac	ccg	ccc	ggc	gac	ccg	aac	384
Ile	Arg	Asn	Met	Leu	Ala	Val	Arg	Gly	Asp	Pro	Pro	Gly	Asp	Pro	Asn	
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Ala	Asp	Trp	Ile	Ala	His	Pro	Glu	Gly	Leu	Thr	Tyr	Ala	Ala	Glu	Leu	
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Phe	Pro	Glu	Met	His	Pro	Arg	Ser	Ala	Asp	Trp	Asp	Thr	Asp	Val	Thr	
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Met	Phe	Phe	Gln	Pro	Asp	Ser	Tyr	Leu	Arg	Leu	Arg	Asp	Arg	Val	Ala	
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gcg	gcc	ggc	tgc	gcg	acc	ccg	gtc	atc	ccc	gag	gtc	atg	ccg	gtg	acc	672
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Ser	Val	Lys	Met	Leu	Glu	Arg	Leu	Pro	Lys	Leu	Ser	Asn	Ala	Ser	Phe	
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ccg	gcg	gag	ttg	aaa	gag	cgg	atc	ctc	aca	gcc	aag	gac	gat	ccg	gcg	768
Pro	Ala	Glu	Leu	Lys	Glu	Arg	Ile	Leu	Thr	Ala	Lys	Asp	Asp	Pro	Ala	
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gct	gta	cgc	tcg	atc	ggc	atc	gag	ttc	gcc	acg	gag	ttc	tgc	gcg	cgg	816
Ala	Val	Arg	Ser	Ile	Gly	Ile	Glu	Phe	Ala	Thr	Glu	Phe	Cys	Ala	Arg	
			260				265						270			
ctg	ctg	gcc	gag	gga	gtg	cca	gga	ctg	cac	ttc	atc	acg	ctc	aac	aac	864
Leu	Leu	Ala	Glu	Gly	Val	Pro	Gly	Leu	His	Phe	Ile	Thr	Leu	Asn	Asn	
		275					280					285				
tcc	acg	gcg	acg	ctg	gaa	atc	tac	gag	aac	ctg	ggc	ctg	cac	cac	cca	912
Ser	Thr	Ala	Thr	Leu	Glu	Ile	Tyr	Glu	Asn	Leu	Gly	Leu	His	His	Pro	
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Pro Arg Ala
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<213> Streptomyces coelicolor

<400> 6

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Ala	Pro	Lys	Thr	Pro	Lys	Gly	Glu	Arg	Asn	Leu	Trp	Ser	Ala	Leu	Arg	35	40	45	
Arg	Val	Glu	Ala	Val	Ala	Pro	Asp	Phe	Val	Ser	Val	Thr	Tyr	Gly	Ala	50	55	60	
Gly	Gly	Ser	Thr	Arg	Ala	Gly	Thr	Val	Arg	Glu	Thr	Gln	Gln	Ile	Val	65	70	75	80
Ala	Asp	Thr	Thr	Leu	Thr	Pro	Val	Ala	His	Leu	Thr	Ala	Val	Asp	His	85	90	95	
Ser	Val	Ala	Glu	Leu	Arg	Asn	Ile	Ile	Gly	Gln	Tyr	Ala	Asp	Ala	Gly	100	105	110	
Ile	Arg	Asn	Met	Leu	Ala	Val	Arg	Gly	Asp	Pro	Pro	Gly	Asp	Pro	Asn	115	120	125	
Ala	Asp	Trp	Ile	Ala	His	Pro	Glu	Gly	Leu	Thr	Tyr	Ala	Ala	Glu	Leu	130	135	140	
Val	Arg	Leu	Ile	Lys	Glu	Ser	Gly	Asp	Phe	Cys	Val	Gly	Val	Ala	Ala	145	150	155	160
Phe	Pro	Glu	Met	His	Pro	Arg	Ser	Ala	Asp	Trp	Asp	Thr	Asp	Val	Thr	165	170	175	
Asn	Phe	Val	Asp	Lys	Cys	Arg	Ala	Gly	Ala	Asp	Tyr	Ala	Ile	Thr	Gln	180	185	190	
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Ala	Ala	Gly	Cys	Ala	Thr	Pro	Val	Ile	Pro	Glu	Val	Met	Pro	Val	Thr	210	215	220	
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Pro	Ala	Glu	Leu	Lys	Glu	Arg	Ile	Leu	Thr	Ala	Lys	Asp	Asp	Pro	Ala	245	250	255	
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 gag ttc ttt cca ccg aag act gaa gag gga gaa aga cag ctc ttt gaa 96
 Glu Phe Phe Pro Pro Lys Thr Glu Glu Gly Glu Arg Gln Leu Phe Glu
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 act ata agg aaa ctt gag aaa tta aat cct act ttt gta tcc gtt act 144
 Thr Ile Arg Lys Leu Glu Lys Leu Asn Pro Thr Phe Val Ser Val Thr
 35 40 45
 tac ggg gca ggt ggt tcg act aga gat aga act agg aat ata gta cag 192
 Tyr Gly Ala Gly Gly Ser Thr Arg Asp Arg Thr Arg Asn Ile Val Gln
 50 55 60
 aaa ata cac gag gaa act aac ctc acc gtt atg gca cac ctc acc tgt 240
 Lys Ile His Glu Glu Thr Asn Leu Thr Val Met Ala His Leu Thr Cys
 65 70 75 80
 ata gca cac acg aga gag gag ctt att gat atc ctt caa gat tac aaa 288
 Ile Ala His Thr Arg Glu Glu Leu Ile Asp Ile Leu Gln Asp Tyr Lys
 85 90 95
 aac ata ggt ata gag aac att ctc gct ttg agg ggg gac gtt ccg agg 336
 Asn Ile Gly Ile Glu Asn Ile Leu Ala Leu Arg Gly Asp Val Pro Arg
 100 105 110
 gac aaa ccg gac tgg aga ccg ccg aag ggt gcg tgc aag tat gca aaa 384
 Asp Lys Pro Asp Trp Arg Pro Pro Lys Gly Ala Cys Lys Tyr Ala Lys
 115 120 125
 gag ctc gta gaa ctg atc agg aag gag ttc gga gac tgg ttt tct atc 432
 Glu Leu Val Glu Leu Ile Arg Lys Glu Phe Gly Asp Trp Phe Ser Ile
 130 135 140
 gga gtg gct tct tat cct gaa gga cat ccg gaa tca ccg aac ctc gag 480
 Gly Val Ala Ser Tyr Pro Glu Gly His Pro Glu Ser Pro Asn Leu Glu
 145 150 155 160

tgg gaa gtg aag tac ttt aag gaa aag gta gag gca ggt gca gac ttc	528
Trp Glu Val Lys Tyr Phe Lys Glu Lys Val Glu Ala Gly Ala Asp Phe	
165 170 175	
tcg att act cag atg ttt ttc gtg aac gat tac tac tac agg ttt gtg	576
Ser Ile Thr Gln Met Phe Phe Val Asn Asp Tyr Tyr Tyr Arg Phe Val	
180 185 190	
gaa atg tgc aaa aat gca ggg ata gat ata tct ata att ccg gga att	624
Glu Met Cys Lys Asn Ala Gly Ile Asp Ile Ser Ile Ile Pro Gly Ile	
195 200 205	
atg cct att act aac ttc aaa cag ata aga aag ttt gct tct ctt tgc	672
Met Pro Ile Thr Asn Phe Lys Gln Ile Arg Lys Phe Ala Ser Leu Cys	
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Gly Ala Thr Ile Pro Gln Ser Leu Ile Glu Lys Leu Glu Lys Val Glu	
225 230 235 240	
gat aaa ccg gaa gaa gta aaa aag ata ggg att gag ttt gcc ata aat	768
Asp Lys Pro Glu Glu Val Lys Lys Ile Gly Ile Glu Phe Ala Ile Asn	
245 250 255	
cag tgt ttg gat ctc ata gaa cac gga gtt ccg ggg ctt cac ttc tac	816
Gln Cys Leu Asp Leu Ile Glu His Gly Val Pro Gly Leu His Phe Tyr	
260 265 270	
act ctg aac aag tcc gac gca act ttg aag ata tac gag gct ata aag	864
Thr Leu Asn Lys Ser Asp Ala Thr Leu Lys Ile Tyr Glu Ala Ile Lys	
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Asp Lys Ile Pro Ala Arg Ser Thr	
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<211> 296

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<213> Aquifex aeolicus

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Tyr Gly Ala Gly Gly Ser Thr Arg Asp Arg Thr Arg Asn Ile Val Gln	
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Lys Ile His Glu Glu Thr Asn Leu Thr Val Met Ala His Leu Thr Cys	
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Ile Ala His Thr Arg Glu Glu Leu Ile Asp Ile Leu Gln Asp Tyr Lys	
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Asn Ile Gly Ile Glu Asn Ile Leu Ala Leu Arg Gly Asp Val Pro Arg
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 Asp Lys Pro Asp Trp Arg Pro Pro Lys Gly Ala Cys Lys Tyr Ala Lys
 115 120 125
 Glu Leu Val Glu Leu Ile Arg Lys Glu Phe Gly Asp Trp Phe Ser Ile
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 Gly Val Ala Ser Tyr Pro Glu Gly His Pro Glu Ser Pro Asn Leu Glu
 145 150 155 160
 Trp Glu Val Lys Tyr Phe Lys Glu Lys Val Glu Ala Gly Ala Asp Phe
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 Ser Ile Thr Gln Met Phe Phe Val Asn Asp Tyr Tyr Tyr Arg Phe Val
 180 185 190
 Glu Met Cys Lys Asn Ala Gly Ile Asp Ile Ser Ile Ile Pro Gly Ile
 195 200 205
 Met Pro Ile Thr Asn Phe Lys Gln Ile Arg Lys Phe Ala Ser Leu Cys
 210 215 220
 Gly Ala Thr Ile Pro Gln Ser Leu Ile Glu Lys Leu Glu Lys Val Glu
 225 230 235 240
 Asp Lys Pro Glu Glu Val Lys Lys Ile Gly Ile Glu Phe Ala Ile Asn
 245 250 255
 Gln Cys Leu Asp Leu Ile Glu His Gly Val Pro Gly Leu His Phe Tyr
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 Asp Lys Ile Pro Ala Arg Ser Thr
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 Glu Gly Val Asp Lys Leu Arg Ala Thr Arg Ala Gln Leu Ala Thr Leu
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 aag ccc aag ttc gtg tcc gtc acg ttc ggc gcc ggc ggc tcg acg caa 144

Lys	Pro	Lys	Phe	Val	Ser	Val	Thr	Phe	Gly	Ala	Gly	Gly	Ser	Thr	Gln	
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cag	ggc	acg	ctc	gac	acc	gtc	gtc	gat	atg	gcg	aag	gaa	ggg	ctc	gaa	192
Gln	Gly	Thr	Leu	Asp	Thr	Val	Val	Asp	Met	Ala	Lys	Glu	Gly	Leu	Glu	
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Ala	Ala	Pro	His	Val	Ser	Cys	Ile	Gly	Ser	Ser	Lys	Glu	Ser	Leu	Arg	
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gcc	att	ctc	aac	gag	tac	cgc	gca	cat	ggc	atc	cgc	cat	atc	gtc	gcg	288
Ala	Ile	Leu	Asn	Glu	Tyr	Arg	Ala	His	Gly	Ile	Arg	His	Ile	Val	Ala	
			85						90					95		
ctg	cgc	ggc	gat	ctg	ccg	tcc	ggc	atg	ggc	gaa	gtc	ggc	gag	ctg	cgc	336
Leu	Arg	Gly	Asp	Leu	Pro	Ser	Gly	Met	Gly	Glu	Val	Gly	Glu	Leu	Arg	
			100					105					110			
tat	gcg	tcg	gaa	ctg	gtg	agc	ttt	atc	cgc	gcc	gaa	ttc	ggc	gac	tgg	384
Tyr	Ala	Ser	Glu	Leu	Val	Ser	Phe	Ile	Arg	Ala	Glu	Phe	Gly	Asp	Trp	
		115					120					125				
ttc	tgc	atc	gag	gtg	gcc	ggc	tat	ccg	gaa	tac	cac	ccg	cag	tcg	cgc	432
Phe	Cys	Ile	Glu	Val	Ala	Gly	Tyr	Pro	Glu	Tyr	His	Pro	Gln	Ser	Arg	
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Ser	Pro	Arg	Gln	Asp	Leu	Glu	Asn	Phe	Ala	Arg	Lys	Val	Lys	Ala	Gly	
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Ala	Asn	Ser	Ala	Ile	Thr	Gln	Tyr	Phe	Phe	Asn	Ala	Asp	Ala	Tyr	Phe	
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cgt	ttc	gtc	gac	gac	gcg	aga	aag	ctc	ggc	gtg	gac	gtg	ccg	atc	gtg	576
Arg	Phe	Val	Asp	Asp	Ala	Arg	Lys	Leu	Gly	Val	Asp	Val	Pro	Ile	Val	
			180					185					190			
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Pro	Gly	Ile	Met	Pro	Ile	Thr	Asn	Phe	Ser	Gln	Leu	Met	Arg	Phe	Ser	
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Glu	Met	Cys	Gly	Ala	Glu	Val	Pro	Arg	Trp	Ile	Ala	Arg	Arg	Leu	Glu	
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Ser	Phe	Gly	Asp	Asp	Arg	Glu	Ser	Ile	Arg	Ala	Phe	Gly	Leu	Asp	Val	
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gtg	acg	gac	ctg	tgc	agg	cgt	ctg	atc	gat	gcg	aag	gtg	ccg	ggc	ctg	768
Val	Thr	Asp	Leu	Cys	Arg	Arg	Leu	Ile	Asp	Ala	Lys	Val	Pro	Gly	Leu	
				245					250					255		
cac	ttc	tac	acg	cta	aac	ggc	gca	gcg	gcg	acc	aag	gcg	atc	tgc	gaa	816
His	Phe	Tyr	Thr	Leu	Asn	Gly	Ala	Ala	Ala	Thr	Lys	Ala	Ile	Cys	Glu	
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Arg Leu Asn Val
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35 40 45
Gln Gly Thr Leu Asp Thr Val Val Asp Met Ala Lys Glu Gly Leu Glu
50 55 60
Ala Ala Pro His Val Ser Cys Ile Gly Ser Ser Lys Glu Ser Leu Arg
65 70 75 80
Ala Ile Leu Asn Glu Tyr Arg Ala His Gly Ile Arg His Ile Val Ala
85 90 95
Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Glu Val Gly Glu Leu Arg
100 105 110
Tyr Ala Ser Glu Leu Val Ser Phe Ile Arg Ala Glu Phe Gly Asp Trp
115 120 125
Phe Cys Ile Glu Val Ala Gly Tyr Pro Glu Tyr His Pro Gln Ser Arg
130 135 140
Ser Pro Arg Gln Asp Leu Glu Asn Phe Ala Arg Lys Val Lys Ala Gly
145 150 155 160
Ala Asn Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe
165 170 175
Arg Phe Val Asp Asp Ala Arg Lys Leu Gly Val Asp Val Pro Ile Val
180 185 190
Pro Gly Ile Met Pro Ile Thr Asn Phe Ser Gln Leu Met Arg Phe Ser
195 200 205
Glu Met Cys Gly Ala Glu Val Pro Arg Trp Ile Ala Arg Arg Leu Glu
210 215 220
Ser Phe Gly Asp Asp Arg Glu Ser Ile Arg Ala Phe Gly Leu Asp Val
225 230 235 240
Val Thr Asp Leu Cys Arg Arg Leu Ile Asp Ala Lys Val Pro Gly Leu
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His Phe Tyr Thr Leu Asn Gly Ala Ala Ala Thr Lys Ala Ile Cys Glu
260 265 270

Arg Leu Asn Val
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Pro Pro Gln Thr Pro Glu Gly Met Glu Lys Leu Arg Ala Thr Arg Ile	
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Gln Leu Ala Gln Phe Asn Pro Lys Phe Phe Ser Val Thr Phe Gly Ala	
35 40 45	
ggc gga tcc act cgt gaa cgc acg ctc gaa acc gtg ctg gaa att cag	192
Gly Gly Ser Thr Arg Glu Arg Thr Leu Glu Thr Val Leu Glu Ile Gln	
50 55 60	
gca gaa ggc tat ccg gta gcg ccc cat ctt tcc tgt atc ggc tcc acg	240
Ala Glu Gly Tyr Pro Val Ala Pro His Leu Ser Cys Ile Gly Ser Thr	
65 70 75 80	
cgt gac aat atc cgt tcg atc ctt gag aaa tat cac agt cac ggt atc	288
Arg Asp Asn Ile Arg Ser Ile Leu Glu Lys Tyr His Ser His Gly Ile	
85 90 95	
agc cgc att gtg gcg cta cgt ggt gat tta ccc tcc ggc atg gcg cag	336
Ser Arg Ile Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Ala Gln	
100 105 110	
gcg gga gaa ttc cgc tac gcc aac gag ctg gta gca ttt atc cgc aag	384
Ala Gly Glu Phe Arg Tyr Ala Asn Glu Leu Val Ala Phe Ile Arg Lys	
115 120 125	
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Glu Phe Gly Asp Thr Phe Trp Ile Glu Val Ala Ala Tyr Pro Glu Tyr	
130 135 140	
cat cca caa gcc cgc tcc gct ctg gag gat ttc acc aat ttc aga cga	480
His Pro Gln Ala Arg Ser Ala Leu Glu Asp Phe Thr Asn Phe Arg Arg	
145 150 155 160	
aaa gtc gaa gca ggt tcc aat gca gcg att acc cag ttt ttc tat aac	528
Lys Val Glu Ala Gly Ser Asn Ala Ala Ile Thr Gln Phe Phe Tyr Asn	
165 170 175	

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Val Asp Ala Tyr Leu His Phe Val Glu Met Cys Glu Ala Ala Asp Leu
180 185 190

aat atc ccg atc gtt ccc ggc atc atg ccg atc agc aaa ttt tct caa 624
Asn Ile Pro Ile Val Pro Gly Ile Met Pro Ile Ser Lys Phe Ser Gln
195 200 205

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210 215 220

cgc aga aaa ctg gaa agc ttc ggt gat gat att ccg tct atc cag gca 720
Arg Arg Lys Leu Glu Ser Phe Gly Asp Asp Ile Pro Ser Ile Gln Ala
225 230 235 240

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Phe Gly Leu Asp Val Val Thr Ala Leu Cys Ala Arg Leu Leu Glu Ala
245 250 255

ggc gca ccc ggc ctg cat ttc tac aca ctc aac tcc gcc gta cta ccc 816
Gly Ala Pro Gly Leu His Phe Tyr Thr Leu Asn Ser Ala Val Leu Pro
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35 40 45

Gly Gly Ser Thr Arg Glu Arg Thr Leu Glu Thr Val Leu Glu Ile Gln
50 55 60

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65 70 75 80

Arg Asp Asn Ile Arg Ser Ile Leu Glu Lys Tyr His Ser His Gly Ile
85 90 95

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Ala Gly Glu Phe Arg Tyr Ala Asn Glu Leu Val Ala Phe Ile Arg Lys
115 120 125

Glu Phe Gly Asp Thr Phe Trp Ile Glu Val Ala Ala Tyr Pro Glu Tyr

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Val	Asp	Ala	Tyr	Leu	His	Phe	Val	Glu	Met	Cys	Glu	Ala	Ala	Asp	Leu
			180					185					190		
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Phe	Gly	Leu	Asp	Val	Val	Thr	Ala	Leu	Cys	Ala	Arg	Leu	Leu	Glu	Ala
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Ser	Phe	Glu	Phe	Phe	Pro	Ala	Lys	Thr	Glu	Ala	Gly	His	Glu	Lys	Leu	
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Leu	Ala	Thr	Ala	Arg	Asn	Leu	Ala	Gly	Tyr	Lys	Pro	Asp	Phe	Phe	Ser	
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Cys	Thr	Tyr	Gly	Ala	Gly	Gly	Ser	Thr	Arg	Asp	Arg	Thr	Leu	Ser	Thr	
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Tyr Arg Glu Ala Gly Ile Arg Arg Ile Val Ala Leu Arg Gly Asp Leu	
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ccg tcg ggc atg ggc atg gcc agc ggc gaa ctg cgc tac gcc aac gaa	384
Pro Ser Gly Met Gly Met Ala Ser Gly Glu Leu Arg Tyr Ala Asn Glu	
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Leu Val Asp Phe Ile Arg Thr Glu Thr Gly Asp His Phe His Ile Glu	
130 135 140	
gtc gcc gcc tat ccg gag gtc cac ccc cag gcg cgc agc ttc gag gat	480
Val Ala Ala Tyr Pro Glu Val His Pro Gln Ala Arg Ser Phe Glu Asp	
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gac ctg gcg aac ttc gtg cgc aag gtg aag gcc ggc gcc agc agc gcc	528
Asp Leu Ala Asn Phe Val Arg Lys Val Lys Ala Gly Ala Ser Ser Ala	
165 170 175	
atc acc cag tac ttc ttc aac gcc gat gcc tat ttc tac ttc gtc gag	576
Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe Tyr Phe Val Glu	
180 185 190	
cgg gtc gcc aag ctc ggc gtg gac atc ccg gtg gtc ccc ggc atc atg	624
Arg Val Ala Lys Leu Gly Val Asp Ile Pro Val Val Pro Gly Ile Met	
195 200 205	
ccg atc acc aac tac tcc aag ctg gcg cgc ttc tcc gac gcc tgc ggc	672
Pro Ile Thr Asn Tyr Ser Lys Leu Ala Arg Phe Ser Asp Ala Cys Gly	
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gcc gaa ctg ccg cgc tgg atc cgc aag caa ctg gaa gcc tac ggc gac	720
Ala Glu Leu Pro Arg Trp Ile Arg Lys Gln Leu Glu Ala Tyr Gly Asp	
225 230 235 240	
gac agc cgc agc atc cag gcc ttc ggc gag cag gtc atc agc gag atg	768
Asp Ser Arg Ser Ile Gln Ala Phe Gly Glu Gln Val Ile Ser Glu Met	
245 250 255	
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Cys Glu Arg Leu Leu Glu Gly Gly Ala Pro Gly Leu His Phe Tyr Thr	
260 265 270	
ttg aac cag gcc gat ccg agc ctg gcg atc tgg aag aat ctc cag ctg	864
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Pro Arg	
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<213> *Pseudomonas aeruginosa*

<400> 14

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Cys Thr Tyr Gly Ala Gly Gly Ser Thr Arg Asp Arg Thr Leu Ser Thr
      50           55           60

Val Leu Gln Leu Asp Gly Glu Val Lys Val Pro Thr Ala Pro His Leu
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Ser Cys Val Gly Asp Ser Lys Ala Glu Leu Arg Glu Leu Leu Gly Arg
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Tyr Arg Glu Ala Gly Ile Arg Arg Ile Val Ala Leu Arg Gly Asp Leu
      100           105           110

Pro Ser Gly Met Gly Met Ala Ser Gly Glu Leu Arg Tyr Ala Asn Glu
      115           120           125

Leu Val Asp Phe Ile Arg Thr Glu Thr Gly Asp His Phe His Ile Glu
 130           135           140

Val Ala Ala Tyr Pro Glu Val His Pro Gln Ala Arg Ser Phe Glu Asp
145           150           155           160

Asp Leu Ala Asn Phe Val Arg Lys Val Lys Ala Gly Ala Ser Ser Ala
          165           170           175

Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe Tyr Phe Val Glu
      180           185           190

Arg Val Ala Lys Leu Gly Val Asp Ile Pro Val Val Pro Gly Ile Met
      195           200           205

Pro Ile Thr Asn Tyr Ser Lys Leu Ala Arg Phe Ser Asp Ala Cys Gly
      210           215           220

Ala Glu Leu Pro Arg Trp Ile Arg Lys Gln Leu Glu Ala Tyr Gly Asp
225           230           235           240

Asp Ser Arg Ser Ile Gln Ala Phe Gly Glu Gln Val Ile Ser Glu Met
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Cys Glu Arg Leu Leu Glu Gly Gly Ala Pro Gly Leu His Phe Tyr Thr
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Pro Arg
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 20 25 30

gaa tac gtc tcc tgc acc ttc ggc gcc ggt ggc tcc aca ctc agt tac 144
 Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr
 35 40 45

acc tca gaa aca gtg cgc cat ctc agc caa cac cac ggc ttt gac gcc 192
 Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Ala
 50 55 60

gca ccg cat ctg tcc tgt gtg ggc ggc agt cgc caa gaa atc cgc gaa 240
 Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu
 65 70 75 80

ctt ctc aaa ctg tac cgc gcg att ggc tgc caa cgc atc gtg gcg cta 288
 Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu
 85 90 95

cgc ggc gat ctc ccc tcg ggc atg ggc cac ccc ggc gac ctc cgc tac 336
 Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr
 100 105 110

gca gct gac ctg att acc ttc atc cgt acc gag cat ggc gat cac ttc 384
 Ala Ala Asp Leu Ile Thr Phe Ile Arg Thr Glu His Gly Asp His Phe
 115 120 125

cac cta gag atc ggc gca tac ccg gaa acc cac cca caa gcc agc aac 432
 His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn
 130 135 140

aca ctg aac gac ctt cac tat ttc aaa gcc aaa gcc gat gca ggc gcc 480
 Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala
 145 150 155 160

gat gcg gca atc act caa tac ttt tat aac cca gac gcc tat ttc cac 528
 Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His
 165 170 175

ttc gtc gac gca gtg cag cgc ctg ggc gtc acc atc ccc att gtt gcc 576
 Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala
 180 185 190

gga gtc atg ccc atc tcc aac ttt gac cag ttg cgc cat ttc tcc gaa 624

Gly	Val	Met	Pro	Ile	Ser	Asn	Phe	Asp	Gln	Leu	Arg	His	Phe	Ser	Glu		
		195					200					205					
caa	tgc	ggc	gcc	gaa	ata	ccc	cgc	tgg	att	aca	aaa	aaa	atg	cag	gct	672	
Gln	Cys	Gly	Ala	Glu	Ile	Pro	Arg	Trp	Ile	Thr	Lys	Lys	Met	Gln	Ala		
	210					215					220						
tac	ggc	gac	gac	acc	aaa	tcg	ata	cgc	gcg	ttc	ggt	gcc	gac	gtc	gtg	720	
Tyr	Gly	Asp	Asp	Thr	Lys	Ser	Ile	Arg	Ala	Phe	Gly	Ala	Asp	Val	Val		
225					230					235					240		
acc	gca	tta	tgt	gag	cgg	cta	atc	gct	ggc	ggc	gca	ccg	ggg	ctg	cac	768	
Thr	Ala	Leu	Cys	Glu	Arg	Leu	Ile	Ala	Gly	Gly	Ala	Pro	Gly	Leu	His		
				245					250					255			
ttc	tac	acg	ctc	aac	cta	gcc	aaa	cca	agc	acc	caa	gtg	ctg	caa	cgc	816	
Phe	Tyr	Thr	Leu	Asn	Leu	Ala	Lys	Pro	Ser	Thr	Gln	Val	Leu	Gln	Arg		
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tta	ggc	tat	tga													828	
Leu	Gly	Tyr															
		275															

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 <212> PRT
 <213> Xylella almond

<400> 16																	
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Glu	Tyr	Val	Ser	Cys	Thr	Phe	Gly	Ala	Gly	Gly	Ser	Thr	Leu	Ser	Tyr		
		35					40					45					
Thr	Ser	Glu	Thr	Val	Arg	His	Leu	Ser	Gln	His	His	Gly	Phe	Asp	Ala		
		50					55					60					
Ala	Pro	His	Leu	Ser	Cys	Val	Gly	Gly	Ser	Arg	Gln	Glu	Ile	Arg	Glu		
65					70				75						80		
Leu	Leu	Lys	Leu	Tyr	Arg	Ala	Ile	Gly	Cys	Gln	Arg	Ile	Val	Ala	Leu		
				85					90					95			
Arg	Gly	Asp	Leu	Pro	Ser	Gly	Met	Gly	His	Pro	Gly	Asp	Leu	Arg	Tyr		
		100						105					110				
Ala	Ala	Asp	Leu	Ile	Thr	Phe	Ile	Arg	Thr	Glu	His	Gly	Asp	His	Phe		
		115					120					125					
His	Leu	Glu	Ile	Gly	Ala	Tyr	Pro	Glu	Thr	His	Pro	Gln	Ala	Ser	Asn		
		130				135					140						
Thr	Leu	Asn	Asp	Leu	His	Tyr	Phe	Lys	Ala	Lys	Ala	Asp	Ala	Gly	Ala		
145					150					155					160		

Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His
 165 170 175
 Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala
 180 185 190
 Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu
 195 200 205
 Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala
 210 215 220
 Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val
 225 230 235 240
 Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His
 245 250 255
 Phe Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg
 260 265 270
 Leu Gly Tyr
 275

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 <211> 828
 <212> DNA
 <213> Xylella oleander

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 <222> (1)..(825)
 <223> RXFY01676

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 cgc gca cag ttg gac agg aca gca aac cgg cta cgc gca ttc gca cca 96
 Arg Ala Gln Leu Asp Arg Thr Ala Asn Arg Leu Arg Ala Phe Ala Pro
 20 25 30

 gaa tac gtc tcc tgc acc ttc ggc gcc ggc ggc tcc aca ctc agt tac 144
 Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr
 35 40 45

 acc tca gaa aca gtg cgc cat ctc agt caa cac cac ggc ttt gac acc 192
 Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Thr
 50 55 60

 gca ccg cat ctg tcc tgt gtg ggc ggc agt cgc caa gaa atc cgc gaa 240
 Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu
 65 70 75 80

 ctt ctc aaa ctg tac cgc gcg att ggc tgc caa cgc atc gtg gcg cta 288
 Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu
 85 90 95

cgc ggc gat ctc ccc tcg ggc atg ggc cac ccc ggc gac ctc cgc tac 336
 Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr
 100 105 110

gca gct gac ctg att acc ttc atc cgt gcc gag cat ggc gat cac ttc 384
 Ala Ala Asp Leu Ile Thr Phe Ile Arg Ala Glu His Gly Asp His Phe
 115 120 125

cac cta gag atc ggc gca tac ccg gaa acc cac cca caa gcc agc aac 432
 His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn
 130 135 140

aca ctg aac gac ctt cac tat ttc aaa gcc aaa gcc gat gca ggc gcc 480
 Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala
 145 150 155 160

gat gcg gca atc act caa tac ttt tac aac cca gac gcc tat ttc cac 528
 Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His
 165 170 175

ttc gtc gac gca gtg cag cgc ctg ggc gtc acc atc ccc att gtt gcc 576
 Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala
 180 185 190

gga gtc atg ccc atc tcc aac ttt gac cag ttg cgc cat ttc tcc gaa 624
 Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu
 195 200 205

caa tgc ggc gcc gaa ata ccc cgc tgg att aca aaa aaa atg cag gct 672
 Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala
 210 215 220

tac ggc gat gac acc aaa tcg ata cgc gcg ttc ggt gcc gac gtc gtg 720
 Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val
 225 230 235 240

acc gca cta tgt gag cgg cta atc gct ggc ggc gca ccg ggg ctg cac 768
 Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His
 245 250 255

ttc tac acg ctc aac cta gcc aaa cca agc acc caa gtg ctg caa cgc 816
 Phe Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg
 260 265 270

tta ggc tat tga 828
 Leu Gly Tyr
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<210> 18

<211> 275

<212> PRT

<213> Xylella oleander

<400> 18

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 20 25 30
 Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr
 35 40 45
 Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Thr
 50 55 60
 Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu
 65 70 75 80
 Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu
 85 90 95
 Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr
 100 105 110
 Ala Ala Asp Leu Ile Thr Phe Ile Arg Ala Glu His Gly Asp His Phe
 115 120 125
 His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn
 130 135 140
 Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala
 145 150 155 160
 Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His
 165 170 175
 Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala
 180 185 190
 Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu
 195 200 205
 Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala
 210 215 220
 Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val
 225 230 235 240
 Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His
 245 250 255
 Phe Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg
 260 265 270
 Leu Gly Tyr
 275

<210> 19

<211> 846

<212> DNA

<213> *Pseudomonas fluorescens*

<220>

<221> CDS

<222> (1)..(843)

<223> RPU04845

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gat gct ggg cat gaa aaa ctg ctc gcc act gcc cgt cag ctg gcc acc	96
Asp Ala Gly His Glu Lys Leu Leu Ala Thr Ala Arg Gln Leu Ala Thr	
20 25 30	
tat aag cct gac ttc ttt tcc tgc acc tac ggc gct ggc ggt tcg acc	144
Tyr Lys Pro Asp Phe Phe Ser Cys Thr Tyr Gly Ala Gly Gly Ser Thr	
35 40 45	
cgt gac cgc acg ctg aac acc gtt ctg cag ctg gaa agc gaa gtc aaa	192
Arg Asp Arg Thr Leu Asn Thr Val Leu Gln Leu Glu Ser Glu Val Lys	
50 55 60	
atc ccc gcc gca ccg cac ctg tcg tgc gtc ggc gac agc aag gac gac	240
Ile Pro Ala Ala Pro His Leu Ser Cys Val Gly Asp Ser Lys Asp Asp	
65 70 75 80	
ctg cgc ggc ctg ctg aac gag tac aag gcc gcc ggc atc aag cgc atc	288
Leu Arg Gly Leu Leu Asn Glu Tyr Lys Ala Ala Gly Ile Lys Arg Ile	
85 90 95	
gtc gcc ctg cgc ggt gac ctg ccg tcc ggc atg ggc atg acc agc ggc	336
Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Met Thr Ser Gly	
100 105 110	
gag ctg cgt cac gcc aat gaa ctg gtt gaa ttc att cgt gaa gaa acc	384
Glu Leu Arg His Ala Asn Glu Leu Val Glu Phe Ile Arg Glu Glu Thr	
115 120 125	
ggc aat cat ttc cac atc gaa gtc gcc gcc tac ccg gag atg cat ccg	432
Gly Asn His Phe His Ile Glu Val Ala Ala Tyr Pro Glu Met His Pro	
130 135 140	
caa gcg cgc aac tac gaa gac gat ctc gcc aac ttc gtg cgc aag gcc	480
Gln Ala Arg Asn Tyr Glu Asp Asp Leu Ala Asn Phe Val Arg Lys Ala	
145 150 155 160	
cgt gcc ggc gcc gac agc gcg atc acc cag tac ttc ttc aac gcc gac	528
Arg Ala Gly Ala Asp Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp	
165 170 175	
agc tac ttc tac ttc gtc gac cgt ttg cag gcg ctg ggc gtg gac att	576
Ser Tyr Phe Tyr Phe Val Asp Arg Leu Gln Ala Leu Gly Val Asp Ile	
180 185 190	
ccg gtg gta ccg ggg atc atg ccg atc acc aac tac agc aaa ctc gcg	624
Pro Val Val Pro Gly Ile Met Pro Ile Thr Asn Tyr Ser Lys Leu Ala	
195 200 205	
cgc ttc tcc gat gcc tgc ggt gcg gaa atc ccg cgc tgg atc cgc aag	672
Arg Phe Ser Asp Ala Cys Gly Ala Glu Ile Pro Arg Trp Ile Arg Lys	
210 215 220	
cag ctg gaa gcc tac ggc gat gac agc caa agc att cag cgc ttt ggc	720
Gln Leu Glu Ala Tyr Gly Asp Asp Ser Gln Ser Ile Gln Arg Phe Gly	

25

225	230	235	240	
gaa caa gtc gtc acg gaa atg tgc gaa cgc ctg ctg caa ggc ggc gcg				768
Glu Gln Val Val Thr Glu Met Cys Glu Arg Leu Leu Gln Gly Gly Ala	245	250	255	
ccc ggc ctg cac ttc tat tcc atg aac cag gcc gaa cca agc ctg gcg				816
Pro Gly Leu His Phe Tyr Ser Met Asn Gln Ala Glu Pro Ser Leu Ala	260	265	270	
atc tgg aac aac ctg aag ctg ccg cgc taa				846
Ile Trp Asn Asn Leu Lys Leu Pro Arg	275	280		

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<211> 281

<212> PRT

<213> *Pseudomonas fluorescens*

. <400> 20

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Tyr Lys Pro Asp Phe Phe Ser Cys Thr Tyr Gly Ala Gly Gly Ser Thr	35	40	45	
Arg Asp Arg Thr Leu Asn Thr Val Leu Gln Leu Glu Ser Glu Val Lys	50	55	60	
Ile Pro Ala Ala Pro His Leu Ser Cys Val Gly Asp Ser Lys Asp Asp	65	70	75	80
Leu Arg Gly Leu Leu Asn Glu Tyr Lys Ala Ala Gly Ile Lys Arg Ile	85	90	95	
Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Met Thr Ser Gly	100	105	110	
Glu Leu Arg His Ala Asn Glu Leu Val Glu Phe Ile Arg Glu Glu Thr	115	120	125	
Gly Asn His Phe His Ile Glu Val Ala Ala Tyr Pro Glu Met His Pro	130	135	140	
Gln Ala Arg Asn Tyr Glu Asp Asp Leu Ala Asn Phe Val Arg Lys Ala	145	150	155	160
Arg Ala Gly Ala Asp Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp	165	170	175	
Ser Tyr Phe Tyr Phe Val Asp Arg Leu Gln Ala Leu Gly Val Asp Ile	180	185	190	
Pro Val Val Pro Gly Ile Met Pro Ile Thr Asn Tyr Ser Lys Leu Ala	195	200	205	
Arg Phe Ser Asp Ala Cys Gly Ala Glu Ile Pro Arg Trp Ile Arg Lys				

210	215	220	
Gln Leu Glu Ala Tyr Gly Asp Asp Ser Gln Ser Ile Gln Arg Phe Gly			
225	230	235	240
Glu Gln Val Val Thr Glu Met Cys Glu Arg Leu Leu Gln Gly Gly Ala			
	245	250	255
Pro Gly Leu His Phe Tyr Ser Met Asn Gln Ala Glu Pro Ser Leu Ala			
	260	265	270
Ile Trp Asn Asn Leu Lys Leu Pro Arg			
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<223> RSO01645			
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1	5	10	15
act tac agt tat gaa ttt ttt cct cca aaa acg agc act ggt gtc caa			96
Thr Tyr Ser Tyr Glu Phe Phe Pro Pro Lys Thr Ser Thr Gly Val Gln			
	20	25	30
aat ctt tac aat cgt ata gat cgc atg aag act tgg ggt cgt ccc atg			144
Asn Leu Tyr Asn Arg Ile Asp Arg Met Lys Thr Trp Gly Arg Pro Met			
	35	40	45
ttt gtc gat gtg act tgg ggt gct ggt ggt act tct tca gaa ctg act			192
Phe Val Asp Val Thr Trp Gly Ala Gly Gly Thr Ser Ser Glu Leu Thr			
	50	55	60
cct gga atc gtt aat gta att caa aca gat ttt gaa gtg gat act tgc			240
Pro Gly Ile Val Asn Val Ile Gln Thr Asp Phe Glu Val Asp Thr Cys			
	65	70	75
atg cat ttg act tgt acg aac atg tcc aca gaa atg att gac gca gct			288
Met His Leu Thr Cys Thr Asn Met Ser Thr Glu Met Ile Asp Ala Ala			
	85	90	95
ttg aaa cgg gct cat gaa aca ggg tgt cgt aac ata ttg gcc ctt aga			336
Leu Lys Arg Ala His Glu Thr Gly Cys Arg Asn Ile Leu Ala Leu Arg			
	100	105	110
ggt gat cct gtt aaa gat aca gac tgg act gaa ggc gaa agt gga ttc			384
Gly Asp Pro Val Lys Asp Thr Asp Trp Thr Glu Gly Glu Ser Gly Phe			
	115	120	125
cgg tat gct tca gac tta gtt aga tat att cgc aca cat tat aat gat			432
Arg Tyr Ala Ser Asp Leu Val Arg Tyr Ile Arg Thr His Tyr Asn Asp			
	130	135	140

gaa ttc tgt att ggt gta gct ggc tat cca gaa gga tat tca cca gat	480
Glu Phe Cys Ile Gly Val Ala Gly Tyr Pro Glu Gly Tyr Ser Pro Asp	
145 150 155 160	
gat gac att gat gaa agc ata aag cat ctg aaa tta aaa gtc gat gaa	528
Asp Asp Ile Asp Glu Ser Ile Lys His Leu Lys Leu Lys Val Asp Glu	
165 170 175	
ggg gct gat ttt atc gtt act caa atg ttt tat gat gta gac aat ttt	576
Gly Ala Asp Phe Ile Val Thr Gln Met Phe Tyr Asp Val Asp Asn Phe	
180 185 190	
atc gca tgg gtc gat aaa gtg cgt gca gca gga ata aat atc cct ata	624
Ile Ala Trp Val Asp Lys Val Arg Ala Ala Gly Ile Asn Ile Pro Ile	
195 200 205	
ttt ccg ggc att atg cct att cag gca tgg gat tcc ttt att cgg aga	672
Phe Pro Gly Ile Met Pro Ile Gln Ala Trp Asp Ser Phe Ile Arg Arg	
210 215 220	
gcg aaa tgg agc ggt gtt aaa att ccc cag cat ttt atg gat act cta	720
Ala Lys Trp Ser Gly Val Lys Ile Pro Gln His Phe Met Asp Thr Leu	
225 230 235 240	
gtc cca gtt aaa gac gat gat gaa gga gtc cgt gag cgt ggt gtt gag	768
Val Pro Val Lys Asp Asp Asp Glu Gly Val Arg Glu Arg Gly Val Glu	
245 250 255	
ctc ata gtc gaa atg tgc cgt aag ctt ata gct agt ggc att acg aga	816
Leu Ile Val Glu Met Cys Arg Lys Leu Ile Ala Ser Gly Ile Thr Arg	
260 265 270	
ctt cat ttt tac act atg aat tta gaa aag gcc gtt aaa atg att att	864
Leu His Phe Tyr Thr Met Asn Leu Glu Lys Ala Val Lys Met Ile Ile	
275 280 285	
gaa cga tta ggt tta tta gat gaa aac ttg gct cct ata gtg gat act	912
Glu Arg Leu Gly Leu Leu Asp Glu Asn Leu Ala Pro Ile Val Asp Thr	
290 295 300	
aat aac gtc gag tta acc aat gct tcc agt caa gat cgt cgg ata aat	960
Asn Asn Val Glu Leu Thr Asn Ala Ser Ser Gln Asp Arg Arg Ile Asn	
305 310 315 320	
gaa ggt gta cgg ccc att ttc tgg cgc act cgt aat gaa agt tat gtc	1008
Glu Gly Val Arg Pro Ile Phe Trp Arg Thr Arg Asn Glu Ser Tyr Val	
325 330 335	
tcg cgt act gat cag tgg gac gaa tta ccg cat ggt cgt tgg ggt gac	1056
Ser Arg Thr Asp Gln Trp Asp Glu Leu Pro His Gly Arg Trp Gly Asp	
340 345 350	
tct cgt agc cct gct ttt ggc gaa ttt gat gct att aga tat ggt ctt	1104
Ser Arg Ser Pro Ala Phe Gly Glu Phe Asp Ala Ile Arg Tyr Gly Leu	
355 360 365	
cgt atg tct ccc aag gag atc aca aca tcg tgg ggg tct cct aaa tct	1152
Arg Met Ser Pro Lys Glu Ile Thr Thr Ser Trp Gly Ser Pro Lys Ser	
370 375 380	

tac	tcg	gaa	atc	ggc	gat	ttg	ttt	gcc	agg	tac	tgt	gaa	aaa	aag	att	1200
Tyr	Ser	Glu	Ile	Gly	Asp	Leu	Phe	Ala	Arg	Tyr	Cys	Glu	Lys	Lys	Ile	
385					390					395					400	
agc	tcc	ctc	cct	tgg	agt	gat	ctt	ccc	ata	tcc	gat	gaa	gcc	gac	ttg	1248
Ser	Ser	Leu	Pro	Trp	Ser	Asp	Leu	Pro	Ile	Ser	Asp	Glu	Ala	Asp	Leu	
				405					410						415	
att	cgg	gat	caa	ctt	cta	agt	atg	aat	aga	aac	gct	ttc	ctt	act	ata	1296
Ile	Arg	Asp	Gln	Leu	Leu	Ser	Met	Asn	Arg	Asn	Ala	Phe	Leu	Thr	Ile	
			420					425						430		
aat	tct	caa	cct	gct	ctt	aac	ggc	gaa	aag	agt	tca	cat	cct	gtt	ttt	1344
Asn	Ser	Gln	Pro	Ala	Leu	Asn	Gly	Glu	Lys	Ser	Ser	His	Pro	Val	Phe	
			435				440						445			
gga	tgg	gga	cca	cct	aat	ggt	tat	gtt	ttc	caa	aaa	cca	tac	gtt	gag	1392
Gly	Trp	Gly	Pro	Pro	Asn	Gly	Tyr	Val	Phe	Gln	Lys	Pro	Tyr	Val	Glu	
	450					455					460					
ttt	ttc	gtt	cac	ccc	tca	ctc	ttg	aat	gaa	ctc	aaa	gaa	acc	gtt	aaa	1440
Phe	Phe	Val	His	Pro	Ser	Leu	Leu	Asn	Glu	Leu	Lys	Glu	Thr	Val	Lys	
465					470				475						480	
aag	ctt	aat	tca	gtt	tcc	tac	ttt	gtt	aca	aac	aag	aat	gga	gac	ttg	1488
Lys	Leu	Asn	Ser	Val	Ser	Tyr	Phe	Val	Thr	Asn	Lys	Asn	Gly	Asp	Leu	
				485					490					495		
gat	acc	aac	tca	caa	tat	gag	att	cca	aat	gcg	gtt	aca	tgg	ggt	gtt	1536
Asp	Thr	Asn	Ser	Gln	Tyr	Glu	Ile	Pro	Asn	Ala	Val	Thr	Trp	Gly	Val	
			500					505					510			
ttc	cct	aat	cgt	gag	att	atc	caa	cct	act	att	gtc	gag	tca	acc	tct	1584
Phe	Pro	Asn	Arg	Glu	Ile	Ile	Gln	Pro	Thr	Ile	Val	Glu	Ser	Thr	Ser	
		515					520					525				
ttt	ctt	gct	tgg	aaa	gat	gaa	gcc	tat	tca	ttg	ggc	atg	gaa	tgg	gct	1632
Phe	Leu	Ala	Trp	Lys	Asp	Glu	Ala	Tyr	Ser	Leu	Gly	Met	Glu	Trp	Ala	
	530					535					540					
aat	gca	tat	agc	cct	gat	tca	att	tct	cgt	aaa	ctt	ttg	gtt	tct	atg	1680
Asn	Ala	Tyr	Ser	Pro	Asp	Ser	Ile	Ser	Arg	Lys	Leu	Leu	Val	Ser	Met	
545					550				555						560	
atg	aag	gaa	tgg	ttc	ctt	tgt	gtc	ata	gtt	gat	aac	gat	ttt	caa	aat	1728
Met	Lys	Glu	Trp	Phe	Leu	Cys	Val	Ile	Val	Asp	Asn	Asp	Phe	Gln	Asn	
				565				570						575		
ggg	caa	tct	ttg	ttt	gat	gtt	ttt	aac	aaa	atg	aga	tct	tta	aaa	gac	1776
Gly	Gln	Ser	Leu	Phe	Asp	Val	Phe	Asn	Lys	Met	Arg	Ser	Leu	Lys	Asp	
			580					585					590			
atc	cat	cct	gag	cta	tat	tat	gca	aat	gca	tca	taa					1812
Ile	His	Pro	Glu	Leu	Tyr	Tyr	Ala	Asn	Ala	Ser						
		595					600									

<210> 22

<211> 603

<212> PRT

<213> Schizosaccharomyces pombe

<400> 22

Met Lys Ile Ser Asp Lys Leu Leu His Pro Asp Trp Lys Glu Lys Val
 1 5 10 15
 Thr Tyr Ser Tyr Glu Phe Phe Pro Pro Lys Thr Ser Thr Gly Val Gln
 20 25 30
 Asn Leu Tyr Asn Arg Ile Asp Arg Met Lys Thr Trp Gly Arg Pro Met
 35 40 45
 Phe Val Asp Val Thr Trp Gly Ala Gly Gly Thr Ser Ser Glu Leu Thr
 50 55 60
 Pro Gly Ile Val Asn Val Ile Gln Thr Asp Phe Glu Val Asp Thr Cys
 65 70 75 80
 Met His Leu Thr Cys Thr Asn Met Ser Thr Glu Met Ile Asp Ala Ala
 85 90 95
 Leu Lys Arg Ala His Glu Thr Gly Cys Arg Asn Ile Leu Ala Leu Arg
 100 105 110
 Gly Asp Pro Val Lys Asp Thr Asp Trp Thr Glu Gly Glu Ser Gly Phe
 115 120 125
 Arg Tyr Ala Ser Asp Leu Val Arg Tyr Ile Arg Thr His Tyr Asn Asp
 130 135 140
 Glu Phe Cys Ile Gly Val Ala Gly Tyr Pro Glu Gly Tyr Ser Pro Asp
 145 150 155 160
 Asp Asp Ile Asp Glu Ser Ile Lys His Leu Lys Leu Lys Val Asp Glu
 165 170 175
 Gly Ala Asp Phe Ile Val Thr Gln Met Phe Tyr Asp Val Asp Asn Phe
 180 185 190
 Ile Ala Trp Val Asp Lys Val Arg Ala Ala Gly Ile Asn Ile Pro Ile
 195 200 205
 Phe Pro Gly Ile Met Pro Ile Gln Ala Trp Asp Ser Phe Ile Arg Arg
 210 215 220
 Ala Lys Trp Ser Gly Val Lys Ile Pro Gln His Phe Met Asp Thr Leu
 225 230 235 240
 Val Pro Val Lys Asp Asp Asp Glu Gly Val Arg Glu Arg Gly Val Glu
 245 250 255
 Leu Ile Val Glu Met Cys Arg Lys Leu Ile Ala Ser Gly Ile Thr Arg
 260 265 270
 Leu His Phe Tyr Thr Met Asn Leu Glu Lys Ala Val Lys Met Ile Ile
 275 280 285
 Glu Arg Leu Gly Leu Leu Asp Glu Asn Leu Ala Pro Ile Val Asp Thr
 290 295 300
 Asn Asn Val Glu Leu Thr Asn Ala Ser Ser Gln Asp Arg Arg Ile Asn
 305 310 315 320

Glu Gly Val Arg Pro Ile Phe Trp Arg Thr Arg Asn Glu Ser Tyr Val
 325 330 335
 Ser Arg Thr Asp Gln Trp Asp Glu Leu Pro His Gly Arg Trp Gly Asp
 340 345 350
 Ser Arg Ser Pro Ala Phe Gly Glu Phe Asp Ala Ile Arg Tyr Gly Leu
 355 360 365
 Arg Met Ser Pro Lys Glu Ile Thr Thr Ser Trp Gly Ser Pro Lys Ser
 370 375 380
 Tyr Ser Glu Ile Gly Asp Leu Phe Ala Arg Tyr Cys Glu Lys Lys Ile
 385 390 395 400
 Ser Ser Leu Pro Trp Ser Asp Leu Pro Ile Ser Asp Glu Ala Asp Leu
 405 410 415
 Ile Arg Asp Gln Leu Leu Ser Met Asn Arg Asn Ala Phe Leu Thr Ile
 420 425 430
 Asn Ser Gln Pro Ala Leu Asn Gly Glu Lys Ser Ser His Pro Val Phe
 435 440 445
 Gly Trp Gly Pro Pro Asn Gly Tyr Val Phe Gln Lys Pro Tyr Val Glu
 450 455 460
 Phe Phe Val His Pro Ser Leu Leu Asn Glu Leu Lys Glu Thr Val Lys
 465 470 475 480
 Lys Leu Asn Ser Val Ser Tyr Phe Val Thr Asn Lys Asn Gly Asp Leu
 485 490 495
 Asp Thr Asn Ser Gln Tyr Glu Ile Pro Asn Ala Val Thr Trp Gly Val
 500 505 510
 Phe Pro Asn Arg Glu Ile Ile Gln Pro Thr Ile Val Glu Ser Thr Ser
 515 520 525
 Phe Leu Ala Trp Lys Asp Glu Ala Tyr Ser Leu Gly Met Glu Trp Ala
 530 535 540
 Asn Ala Tyr Ser Pro Asp Ser Ile Ser Arg Lys Leu Leu Val Ser Met
 545 550 555 560
 Met Lys Glu Trp Phe Leu Cys Val Ile Val Asp Asn Asp Phe Gln Asn
 565 570 575
 Gly Gln Ser Leu Phe Asp Val Phe Asn Lys Met Arg Ser Leu Lys Asp
 580 585 590
 Ile His Pro Glu Leu Tyr Tyr Ala Asn Ala Ser
 595 600

<210> 23

<211> 1800

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1797)

<223> RSC08323

<400> 23

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ccc act tac tca ttc gag tac ttc gtc ccg aag act aca caa ggt gta	96
Pro Thr Tyr Ser Phe Glu Tyr Phe Val Pro Lys Thr Thr Gln Gly Val	
20 25 30	
cag aac ctg tat gac cgg atg gac cgg atg tac gag gct tct ttg ccc	144
Gln Asn Leu Tyr Asp Arg Met Asp Arg Met Tyr Glu Ala Ser Leu Pro	
35 40 45	
caa ttt att gac atc acc tgg aat gca ggc ggt gga cgg ttg tca cat	192
Gln Phe Ile Asp Ile Thr Trp Asn Ala Gly Gly Gly Arg Leu Ser His	
50 55 60	
ctg tcc acg gac ttg gtt gcg aca gcg cag tct gtg ctt ggt ttg gaa	240
Leu Ser Thr Asp Leu Val Ala Thr Ala Gln Ser Val Leu Gly Leu Glu	
65 70 75 80	
acg tgc atg cac ctt acc tgc acc aat atg ccc att tcg atg att gac	288
Thr Cys Met His Leu Thr Cys Thr Asn Met Pro Ile Ser Met Ile Asp	
85 90 95	
gac gct tta gaa aac gct tat cac tcc ggt tgc cag aac atc cta gcg	336
Asp Ala Leu Glu Asn Ala Tyr His Ser Gly Cys Gln Asn Ile Leu Ala	
100 105 110	
ctg aga gga gat cct cct agg gac gca gaa aac tgg act ccc gtt gaa	384
Leu Arg Gly Asp Pro Pro Arg Asp Ala Glu Asn Trp Thr Pro Val Glu	
115 120 125	
ggg ggc ttc cag tat gcc aag gac ttg att aag tat atc aag tcc aag	432
Gly Gly Phe Gln Tyr Ala Lys Asp Leu Ile Lys Tyr Ile Lys Ser Lys	
130 135 140	
tac ggt gac cat ttc gct atc ggc gtt gcc ggc tac ccg gag tgc cat	480
Tyr Gly Asp His Phe Ala Ile Gly Val Ala Gly Tyr Pro Glu Cys His	
145 150 155 160	
ccg gag ttg cct aac aaa gac gtg aag ctt gat ctc gag tat ttg agc	528
Pro Glu Leu Pro Asn Lys Asp Val Lys Leu Asp Leu Glu Tyr Leu Ser	
165 170 175	
aga aga tcg acc ggc ggc gac ttc atc atc act cag atg ttt tac gat	576
Arg Arg Ser Thr Gly Gly Asp Phe Ile Ile Thr Gln Met Phe Tyr Asp	
180 185 190	
gtt gat aat tta ctc aac tgg tgt tcc caa gtt aga gct gcg ggc atg	624
Val Asp Asn Leu Leu Asn Trp Cys Ser Gln Val Arg Ala Ala Gly Met	
195 200 205	
gac gtg ccc att att ccc ggg atc atg ccg atc act acc tac gcg gcc	672
Asp Val Pro Ile Ile Pro Gly Ile Met Pro Ile Thr Thr Tyr Ala Ala	

210	215	220	
ttc ttg aga agg atc caa tgg ggc caa atc tcc atc cct caa cat ttc Phe Leu Arg Arg Ile Gln Trp Gly Gln Ile Ser Ile Pro Gln His Phe 225 230 235 240			720
tcg tcc cga ttg gat cct atc aag gac gat gac gag ttg gtc cgt gat Ser Ser Arg Leu Asp Pro Ile Lys Asp Asp Asp Glu Leu Val Arg Asp 245 250 255			768
atc gga act aac ttg atc gtg gaa atg tgt caa aaa ttg ctc gac agt Ile Gly Thr Asn Leu Ile Val Glu Met Cys Gln Lys Leu Leu Asp Ser 260 265 270			816
ggg tac gtt tct cac ttg cac atc tac acc atg aac ttg gaa aaa gcg Gly Tyr Val Ser His Leu His Ile Tyr Thr Met Asn Leu Glu Lys Ala 275 280 285			864
cct ctc atg att ctg gaa aga ttg aac att cta cct acg gaa tca gag Pro Leu Met Ile Leu Glu Arg Leu Asn Ile Leu Pro Thr Glu Ser Glu 290 295 300			912
ttc aat gca cat cca ttg gcc gtg ttg cca tgg aga aaa tct ttg aat Phe Asn Ala His Pro Leu Ala Val Leu Pro Trp Arg Lys Ser Leu Asn 305 310 315 320			960
cca aag cgt aaa aac gag gaa gtc aga cct atc ttc tgg aag aga aga Pro Lys Arg Lys Asn Glu Glu Val Arg Pro Ile Phe Trp Lys Arg Arg 325 330 335			1008
cct tac tcc tat gtc gca aga acc tct caa tgg gcc gtg gac gaa ttc Pro Tyr Ser Tyr Val Ala Arg Thr Ser Gln Trp Ala Val Asp Glu Phe 340 345 350			1056
ccc aac ggt aga ttc ggt gat tcg tct tct cct gcg ttc ggt gac ttg Pro Asn Gly Arg Phe Gly Asp Ser Ser Ser Pro Ala Phe Gly Asp Leu 355 360 365			1104
gat ctg tgt ggt tca gac ttg atc agg caa tca gcg aac aaa tgt ctc Asp Leu Cys Gly Ser Asp Leu Ile Arg Gln Ser Ala Asn Lys Cys Leu 370 375 380			1152
gaa tta tgg tcc acc cct act tcc atc aac gac gtc gcc ttc ttg gtc Glu Leu Trp Ser Thr Pro Thr Ser Ile Asn Asp Val Ala Phe Leu Val 385 390 395 400			1200
atc aac tac ttg aat gga aac ttg aag tgt tta cct tgg agt gat atc Ile Asn Tyr Leu Asn Gly Asn Leu Lys Cys Leu Pro Trp Ser Asp Ile 405 410 415			1248
ccc atc aat gat gaa ata aat cca atc aaa gca cac ttg att gag ctg Pro Ile Asn Asp Glu Ile Asn Pro Ile Lys Ala His Leu Ile Glu Leu 420 425 430			1296
aac cag cat tct atc atc act ata aac tct caa cct caa gtc aac ggc Asn Gln His Ser Ile Ile Thr Ile Asn Ser Gln Pro Gln Val Asn Gly 435 440 445			1344
att agg tcc aat gac aaa att cat ggt tgg gga ccc aag gat ggt tac Ile Arg Ser Asn Asp Lys Ile His Gly Trp Gly Pro Lys Asp Gly Tyr 450 455 460			1392

gtt tac cag aag caa tat ttg gaa ttt atg ttg ccc aag act aag ttg 1440
 Val Tyr Gln Lys Gln Tyr Leu Glu Phe Met Leu Pro Lys Thr Lys Leu
 465 470 475 480

ccc aag ttg att gac acc ttg aaa aac aat gag ttc ttg acc tac ttc 1488
 Pro Lys Leu Ile Asp Thr Leu Lys Asn Asn Glu Phe Leu Thr Tyr Phe
 485 490 495

gcc atc gac tct caa ggt gac ctg cta agt aat cat cca gac aac tcc 1536
 Ala Ile Asp Ser Gln Gly Asp Leu Leu Ser Asn His Pro Asp Asn Ser
 500 505 510

aag tcc aac gct gtg act tgg ggt att ttc ccc ggc aga gaa att ctt 1584
 Lys Ser Asn Ala Val Thr Trp Gly Ile Phe Pro Gly Arg Glu Ile Leu
 515 520 525

caa cct acc att gtc gag aaa att tcg ttc tta gcg tgg aag gag gag 1632
 Gln Pro Thr Ile Val Glu Lys Ile Ser Phe Leu Ala Trp Lys Glu Glu
 530 535 540

ttc tat cat atc ttg aat gaa tgg aaa cta aac atg aat aaa tac gat 1680
 Phe Tyr His Ile Leu Asn Glu Trp Lys Leu Asn Met Asn Lys Tyr Asp
 545 550 555 560

aaa ccg cat agt gcc caa ttc att cag tcc ttg att gac gat tac tgc 1728
 Lys Pro His Ser Ala Gln Phe Ile Gln Ser Leu Ile Asp Asp Tyr Cys
 565 570 575

ttg gtc aat att gtt gac aat gac tac att tct cca gat gat caa atc 1776
 Leu Val Asn Ile Val Asp Asn Asp Tyr Ile Ser Pro Asp Asp Gln Ile
 580 585 590

cat tcc atc cta cta agc cta taa 1800
 His Ser Ile Leu Leu Ser Leu
 595

<210> 24

<211> 599

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 24

Met Lys Ile Thr Glu Lys Leu Glu Gln His Arg Gln Thr Ser Gly Lys
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Pro Thr Tyr Ser Phe Glu Tyr Phe Val Pro Lys Thr Thr Gln Gly Val
 20 25 30

Gln Asn Leu Tyr Asp Arg Met Asp Arg Met Tyr Glu Ala Ser Leu Pro
 35 40 45

Gln Phe Ile Asp Ile Thr Trp Asn Ala Gly Gly Gly Arg Leu Ser His
 50 55 60

Leu Ser Thr Asp Leu Val Ala Thr Ala Gln Ser Val Leu Gly Leu Glu
 65 70 75 80

Thr Cys Met His Leu Thr Cys Thr Asn Met Pro Ile Ser Met Ile Asp
 85 90 95

Asp Ala Leu Glu Asn Ala Tyr His Ser Gly Cys Gln Asn Ile Leu Ala
 100 105 110
 Leu Arg Gly Asp Pro Pro Arg Asp Ala Glu Asn Trp Thr Pro Val Glu
 115 120 125
 Gly Gly Phe Gln Tyr Ala Lys Asp Leu Ile Lys Tyr Ile Lys Ser Lys
 130 135 140
 Tyr Gly Asp His Phe Ala Ile Gly Val Ala Gly Tyr Pro Glu Cys His
 145 150 155 160
 Pro Glu Leu Pro Asn Lys Asp Val Lys Leu Asp Leu Glu Tyr Leu Ser
 165 170 175
 Arg Arg Ser Thr Gly Gly Asp Phe Ile Ile Thr Gln Met Phe Tyr Asp
 180 185 190
 Val Asp Asn Leu Leu Asn Trp Cys Ser Gln Val Arg Ala Ala Gly Met
 195 200 205
 Asp Val Pro Ile Ile Pro Gly Ile Met Pro Ile Thr Thr Tyr Ala Ala
 210 215 220
 Phe Leu Arg Arg Ile Gln Trp Gly Gln Ile Ser Ile Pro Gln His Phe
 225 230 235 240
 Ser Ser Arg Leu Asp Pro Ile Lys Asp Asp Asp Glu Leu Val Arg Asp
 245 250 255
 Ile Gly Thr Asn Leu Ile Val Glu Met Cys Gln Lys Leu Leu Asp Ser
 260 265 270
 Gly Tyr Val Ser His Leu His Ile Tyr Thr Met Asn Leu Glu Lys Ala
 275 280 285
 Pro Leu Met Ile Leu Glu Arg Leu Asn Ile Leu Pro Thr Glu Ser Glu
 290 295 300
 Phe Asn Ala His Pro Leu Ala Val Leu Pro Trp Arg Lys Ser Leu Asn
 305 310 315 320
 Pro Lys Arg Lys Asn Glu Glu Val Arg Pro Ile Phe Trp Lys Arg Arg
 325 330 335
 Pro Tyr Ser Tyr Val Ala Arg Thr Ser Gln Trp Ala Val Asp Glu Phe
 340 345 350
 Pro Asn Gly Arg Phe Gly Asp Ser Ser Ser Pro Ala Phe Gly Asp Leu
 355 360 365
 Asp Leu Cys Gly Ser Asp Leu Ile Arg Gln Ser Ala Asn Lys Cys Leu
 370 375 380
 Glu Leu Trp Ser Thr Pro Thr Ser Ile Asn Asp Val Ala Phe Leu Val
 385 390 395 400
 Ile Asn Tyr Leu Asn Gly Asn Leu Lys Cys Leu Pro Trp Ser Asp Ile
 405 410 415

Pro Ile Asn Asp Glu Ile Asn Pro Ile Lys Ala His Leu Ile Glu Leu
 420 425 430
 Asn Gln His Ser Ile Ile Thr Ile Asn Ser Gln Pro Gln Val Asn Gly
 435 440 445
 Ile Arg Ser Asn Asp Lys Ile His Gly Trp Gly Pro Lys Asp Gly Tyr
 450 455 460
 Val Tyr Gln Lys Gln Tyr Leu Glu Phe Met Leu Pro Lys Thr Lys Leu
 465 470 475 480
 Pro Lys Leu Ile Asp Thr Leu Lys Asn Asn Glu Phe Leu Thr Tyr Phe
 485 490 495
 Ala Ile Asp Ser Gln Gly Asp Leu Leu Ser Asn His Pro Asp Asn Ser
 500 505 510
 Lys Ser Asn Ala Val Thr Trp Gly Ile Phe Pro Gly Arg Glu Ile Leu
 515 520 525
 Gln Pro Thr Ile Val Glu Lys Ile Ser Phe Leu Ala Trp Lys Glu Glu
 530 535 540
 Phe Tyr His Ile Leu Asn Glu Trp Lys Leu Asn Met Asn Lys Tyr Asp
 545 550 555 560
 Lys Pro His Ser Ala Gln Phe Ile Gln Ser Leu Ile Asp Asp Tyr Cys
 565 570 575
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 580 585 590
 His Ser Ile Leu Leu Ser Leu
 595

<210> 25
 <211> 897
 <212> DNA
 <213> *Erwinia carotovora*

<220>
 <221> CDS
 <222> (1)..(894)
 <223> REO00089

<400> 25
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 1 5 10 15
 gcg gaa ttg cag gga cga att aat gtg tca ttt gaa ttt ttc ccg cca 96
 Ala Glu Leu Gln Gly Arg Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30
 cgt acc agc gat atg gaa gaa acc ctg tgg agc tct atc gat cga ctg 144
 Arg Thr Ser Asp Met Glu Glu Thr Leu Trp Ser Ser Ile Asp Arg Leu
 35 40 45
 agc agc ctg aag ccc aag ttt gtt tcc gtg act tac ggg gcg aat tct 192

Ser	Ser	Leu	Lys	Pro	Lys	Phe	Val	Ser	Val	Thr	Tyr	Gly	Ala	Asn	Ser		
50						55					60						
ggc	gag	cgt	gac	cgt	act	cac	agc	att	atc	aaa	acg	att	aaa	gag	cgt	240	
Gly	Glu	Arg	Asp	Arg	Thr	His	Ser	Ile	Ile	Lys	Thr	Ile	Lys	Glu	Arg	80	
65					70				75								
acc	ggt	ctg	gaa	gcg	gca	cct	cac	ctg	acc	tgc	atc	gat	gct	tca	cgc	288	
Thr	Gly	Leu	Glu	Ala	Ala	Pro	His	Leu	Thr	Cys	Ile	Asp	Ala	Ser	Arg	95	
				85				90									
gaa	cag	ctg	cgt	gaa	atc	gct	cag	gat	tac	tgg	gag	agt	ggt	atc	cgc	336	
Glu	Gln	Leu	Arg	Glu	Ile	Ala	Gln	Asp	Tyr	Trp	Glu	Ser	Gly	Ile	Arg	110	
		100						105									
cat	att	gtc	gcg	ctg	cgc	ggc	gac	ttg	cct	caa	gaa	ggc	ggc	aaa	ccg	384	
His	Ile	Val	Ala	Leu	Arg	Gly	Asp	Leu	Pro	Gln	Glu	Gly	Gly	Lys	Pro	125	
		115					120										
gac	atg	tac	gcg	gcg	gat	ctg	gtt	tcc	ctg	ctg	aaa	gag	gtc	ggt	gat	432	
Asp	Met	Tyr	Ala	Ala	Asp	Leu	Val	Ser	Leu	Leu	Lys	Glu	Val	Gly	Asp	140	
		130				135											
ttc	gat	att	tcc	gtt	gcc	gcc	tat	cct	gaa	gta	cac	cct	gaa	gcg	aaa	480	
Phe	Asp	Ile	Ser	Val	Ala	Ala	Tyr	Pro	Glu	Val	His	Pro	Glu	Ala	Lys	160	
					150				155								
agc	gcg	cag	gct	gac	ctg	att	aac	ctg	aaa	cac	aag	att	gat	gcc	ggc	528	
Ser	Ala	Gln	Ala	Asp	Leu	Ile	Asn	Leu	Lys	His	Lys	Ile	Asp	Ala	Gly	175	
				165				170									
gcg	aat	cgc	gct	atc	aca	cag	ttc	ttt	ttc	gac	gta	gaa	agc	tat	ttg	576	
Ala	Asn	Arg	Ala	Ile	Thr	Gln	Phe	Phe	Phe	Asp	Val	Glu	Ser	Tyr	Leu	190	
			180					185									
cgg	ttc	cgt	gac	cgc	tgc	gtg	gca	acg	ggc	atc	gat	gta	gaa	att	gtg	624	
Arg	Phe	Arg	Asp	Arg	Cys	Val	Ala	Thr	Gly	Ile	Asp	Val	Glu	Ile	Val	205	
		195					200										
ccg	ggc	att	ctg	cca	gta	tcg	aac	ttc	aaa	cag	ttg	cag	aaa	ttt	gcc	672	
Pro	Gly	Ile	Leu	Pro	Val	Ser	Asn	Phe	Lys	Gln	Leu	Gln	Lys	Phe	Ala	220	
		210				215											
acg	atg	acc	aac	gtc	cgt	gtg	ccg	aac	tgg	atg	acg	acc	atg	ttt	gac	720	
Thr	Met	Thr	Asn	Val	Arg	Val	Pro	Asn	Trp	Met	Thr	Thr	Met	Phe	Asp	240	
					230				235								
ggc	ctg	gat	aac	gat	cca	gaa	acc	cgc	aaa	atg	gtg	ggg	gcg	tct	atc	768	
Gly	Leu	Asp	Asn	Asp	Pro	Glu	Thr	Arg	Lys	Met	Val	Gly	Ala	Ser	Ile	255	
				245					250								
gcc	atg	gat	atg	gtg	aaa	att	ctc	agc	cgc	gaa	ggc	gta	aaa	gat	ttc	816	
Ala	Met	Asp	Met	Val	Lys	Ile	Leu	Ser	Arg	Glu	Gly	Val	Lys	Asp	Phe	270	
				260				265									
cat	ttc	tat	acg	ctg	aac	cgc	gcg	gag	ctg	agc	tat	gcg	att	tgc	cat	864	
His	Phe	Tyr	Thr	Leu	Asn	Arg	Ala	Glu	Leu	Ser	Tyr	Ala	Ile	Cys	His	285	
			275				280										
acg	ctg	ggc	gtc	cgc	cct	gat	gta	gca	cgc	tga						897	
Thr	Leu	Gly	Val	Arg	Pro	Asp	Val	Ala	Arg								

290

295

<210> 26

<211> 298

<212> PRT

<213> *Erwinia carotovora*

<400> 26

Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu
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 20 25 30

Arg Thr Ser Asp Met Glu Glu Thr Leu Trp Ser Ser Ile Asp Arg Leu
 35 40 45

Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60

Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Thr Ile Lys Glu Arg
 65 70 75 80

Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg
 85 90 95

Glu Gln Leu Arg Glu Ile Ala Gln Asp Tyr Trp Glu Ser Gly Ile Arg
 100 105 110

His Ile Val Ala Leu Arg Gly Asp Leu Pro Gln Glu Gly Gly Lys Pro
 115 120 125

Asp Met Tyr Ala Ala Asp Leu Val Ser Leu Leu Lys Glu Val Gly Asp
 130 135 140

Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145 150 155 160

Ser Ala Gln Ala Asp Leu Ile Asn Leu Lys His Lys Ile Asp Ala Gly
 165 170 175

Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
 180 185 190

Arg Phe Arg Asp Arg Cys Val Ala Thr Gly Ile Asp Val Glu Ile Val
 195 200 205

Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Leu Gln Lys Phe Ala
 210 215 220

Thr Met Thr Asn Val Arg Val Pro Asn Trp Met Thr Thr Met Phe Asp
 225 230 235 240

Gly Leu Asp Asn Asp Pro Glu Thr Arg Lys Met Val Gly Ala Ser Ile
 245 250 255

Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270

His Phe Tyr Thr Leu Asn Arg Ala Glu Leu Ser Tyr Ala Ile Cys His

275	280	285	
Thr Leu Gly Val Arg Pro Asp Val Ala Arg			
290	295		
<210> 27			
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<220>			
<221> CDS			
<222> (1)..(885)			
<223> RKP07488			
<400> 27			
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Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu			
1 5 10 15			
gcg gaa gtc cag ggc cag att aat gtg tct ttt gaa ttc ttt ccg ccg			96
Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro			
20 25 30			
cgc acc agt gaa atg gag caa acc ctg tgg aaa tcc atc gat cgc ctg			144
Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Lys Ser Ile Asp Arg Leu			
35 40 45			
agc agt ctg aaa ccg aag ttt gtt tgc gta acc tat ggc gcg aac tct			192
Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser			
50 55 60			
ggc gag cgc gat cgc acc cac agc atc atc aaa ggc att aaa gag cga			240
Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Glu Arg			
65 70 75 80			
acc ggt ctg gaa gca gcg ccg cac ctg acc tgt atc gat gcc agc cgc			288
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg			
85 90 95			
gat gag ttg cgc act atc gct cag gat tac tgg aac aac ggt atc cgc			336
Asp Glu Leu Arg Thr Ile Ala Gln Asp Tyr Trp Asn Asn Gly Ile Arg			
100 105 110			
cat atc gtc gcc ctg cgc ggc gac ctg ccg ccg ggc agc ggt aaa ccg			384
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro			
115 120 125			
gat atg tac gcc gcc gat ctg gtg acg ttg ctg aaa gag gta ggc gat			432
Asp Met Tyr Ala Ala Asp Leu Val Thr Leu Leu Lys Glu Val Gly Asp			
130 135 140			
ttt gat atc tct gtc gcc gcg tat ccg gaa gtg cat ccg gag gcg aaa			480
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys			
145 150 155 160			
agc gcg cag gcg gat tta ctg aac ctg aag cgc aaa gta gaa gca ggg			528
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Glu Ala Gly			
165 170 175			

gcc aac cgc gcg atc acc cag ttc ttc ttc gat gtg gaa agc tac ctg 576
 Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
 180 185 190

cgt ttt cgc gat cgc tgc gtc tcg gca ggc atc gac gtg gaa atc att 624
 Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile
 195 200 205

ccc ggt atc ctg ccg gtc tcc aac ttt aaa cag gcg aaa aag ttt gcg 672
 Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
 210 215 220

gat atg acc aac gtc cgt atc ccg gtg tgg atg tca aaa atg ttc gaa 720
 Asp Met Thr Asn Val Arg Ile Pro Val Trp Met Ser Lys Met Phe Glu
 225 230 235 240

ggg ctg gat aac gac gcc gaa acc cgt caa ctg gtg ggg gcg aat atc 768
 Gly Leu Asp Asn Asp Ala Glu Thr Arg Gln Leu Val Gly Ala Asn Ile
 245 250 255

gcc atg gac atg gtg aag atc tta agc cgg gaa ggg gtc aag gat ttc 816
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270

cac ttc tac acc ctg aac cgc gcc gag atg agc tac gcc atc tgc cat 864
 His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
 275 280 285

acg ctg ggc gta cgc ccg gcc tga 888
 Thr Leu Gly Val Arg Pro Ala
 290 295

<210> 28
 <211> 295
 <212> PRT
 <213> *Klebsiella pneumoniae*

<400> 28
 Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu
 1 5 10 15

Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30

Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Lys Ser Ile Asp Arg Leu
 35 40 45

Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60

Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Glu Arg
 65 70 75 80

Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg
 85 90 95

Asp Glu Leu Arg Thr Ile Ala Gln Asp Tyr Trp Asn Asn Gly Ile Arg
 100 105 110

His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro

115					120					125					
Asp	Met	Tyr	Ala	Ala	Asp	Leu	Val	Thr	Leu	Leu	Lys	Glu	Val	Gly	Asp
130					135						140				
Phe	Asp	Ile	Ser	Val	Ala	Ala	Tyr	Pro	Glu	Val	His	Pro	Glu	Ala	Lys
145					150					155					160
Ser	Ala	Gln	Ala	Asp	Leu	Leu	Asn	Leu	Lys	Arg	Lys	Val	Glu	Ala	Gly
				165					170					175	
Ala	Asn	Arg	Ala	Ile	Thr	Gln	Phe	Phe	Phe	Asp	Val	Glu	Ser	Tyr	Leu
			180				185						190		
Arg	Phe	Arg	Asp	Arg	Cys	Val	Ser	Ala	Gly	Ile	Asp	Val	Glu	Ile	Ile
		195					200					205			
Pro	Gly	Ile	Leu	Pro	Val	Ser	Asn	Phe	Lys	Gln	Ala	Lys	Lys	Phe	Ala
	210					215					220				
Asp	Met	Thr	Asn	Val	Arg	Ile	Pro	Val	Trp	Met	Ser	Lys	Met	Phe	Glu
225					230					235					240
Gly	Leu	Asp	Asn	Asp	Ala	Glu	Thr	Arg	Gln	Leu	Val	Gly	Ala	Asn	Ile
				245					250					255	
Ala	Met	Asp	Met	Val	Lys	Ile	Leu	Ser	Arg	Glu	Gly	Val	Lys	Asp	Phe
			260					265					270		
His	Phe	Tyr	Thr	Leu	Asn	Arg	Ala	Glu	Met	Ser	Tyr	Ala	Ile	Cys	His
		275					280					285			
Thr	Leu	Gly	Val	Arg	Pro	Ala									
	290				295										

<210> 29
 <211> 891
 <212> DNA
 <213> Salmonella typhi

<220>
 <221> CDS
 <222> (1)..(888)
 <223> RTY02485

<400> 29																
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Met	Ser	Phe	Phe	His	Ala	Asn	Gln	Arg	Glu	Ala	Leu	Asn	Gln	Ser	Leu	
1				5					10					15		
gcg gaa gta cag ggt cag att aac gtt tcg ttt gaa ttt ttc ccg ccg																96
Ala	Glu	Val	Gln	Gly	Gln	Ile	Asn	Val	Ser	Phe	Glu	Phe	Phe	Pro	Pro	
			20					25					30			
cgc acc agt gaa atg gag caa acc ctg tgg aac tcc atc gat cgc ctg																144
Arg	Thr	Ser	Glu	Met	Glu	Gln	Thr	Leu	Trp	Asn	Ser	Ile	Asp	Arg	Leu	
		35					40					45				
agc agc ctg aaa ccg aag ttt gtt tcg gta acg tat ggc gcc aac tcc																192
Ser	Ser	Leu	Lys	Pro	Lys	Phe	Val	Ser	Val	Thr	Tyr	Gly	Ala	Asn	Ser	

50	55	60	
ggg gaa cgt gac cgc act cat agt gtt att aaa ggc att aaa gag cgt Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg 65 70 75 80			240
act ggg ctt gag gcc gcg ccg cac ctt acc tgt att gac gcc acg cgc Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg 85 90 95			288
gat gaa ctg cgc acc atc gcc cgc gac tac tgg aat aac ggt atc cgc Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg 100 105 110			336
cac att gtt gct ttg cgc ggc gat ttg ccg ccg ggc agc ggt aag ccg His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro 115 120 125			384
gag atg tac gcc gcc gat ctg gtt ggt ttg ctc aaa gag gtg gtc gat Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Val Asp 130 135 140			432
ttc gat att tca gta gcg gcc tat ccg gag gta cat ccg gaa gcg aaa Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys 145 150 155 160			480
agc gcg cag gcc gat ctg ctt aat ctg aag cgt aaa gtg gat gct ggc Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly 165 170 175			528
gct aac cgc gcg ata acc caa ttt ttc ttc gat gtg gaa agc tat ctg Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu 180 185 190			576
cgt ttt cgc gac cgc tgt gtt tcc gcc ggt atc gac gta gaa att att Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile 195 200 205			624
ccc ggc att tta ccg gtg tct aac ttt aaa cag gcg aaa aaa ttt gcc Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala 210 215 220			672
gat atg acc aat gtc cgc att ccg tcc tgg atg tcg ctg atg ttt gag Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu 225 230 235 240			720
ggg ctg gat gat gac gca gaa acc cgc aag ctg gtg ggc gct aac att Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile 245 250 255			768
gcg atg gac atg gtg aaa att tta agc cgc gaa gga gtg aag gat ttc Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe 260 265 270			816
cac ttc tac acg ttg aat cgt gcg gaa atg agt tat gcc att tgc cac His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His 275 280 285			864
acg ctg ggc gta aga ccg ggt tta taa Thr Leu Gly Val Arg Pro Gly Leu 290 295			891

<210> 30
 <211> 296
 <212> PRT
 <213> Salmonella typhi

<400> 30
 Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu
 1 5 10 15
 Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30
 Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
 35 40 45
 Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60
 Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg
 65 70 75 80
 Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg
 85 90 95
 Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg
 100 105 110
 His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
 115 120 125
 Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Val Asp
 130 135 140
 Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145 150 155 160
 Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly
 165 170 175
 Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
 180 185 190
 Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile
 195 200 205
 Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
 210 215 220
 Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu
 225 230 235 240
 Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile
 245 250 255
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270
 His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
 275 280 285

Thr Leu Gly Val Arg Pro Gly Leu
290 295

<210> 31
<211> 891
<212> DNA
<213> Salmonella typhimurium

<220>
<221> CDS
<222> (1)..(888)
<223> RSY00593

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gcg gaa gta cag ggt cag att aac gtt tcg ttt gaa ttt ttc ccg ccg 96
Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
20 25 30
cgc acc agt gaa atg gag caa acc ctg tgg aac tcc atc gat cgc ctg 144
Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
35 40 45
agc agt ctg aaa ccg aag ttt gtt tcg gta acg tat ggc gcc aac tcc 192
Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
50 55 60
ggg gaa cgc gac cgc acc cat agc gtt att aaa ggc atc aaa gag cgt 240
Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg
65 70 75 80
act ggg ctt gag gcc gcg ccg cac ctt acc tgt att gac gcc acg cgc 288
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg
85 90 95
gat gaa ctg cgc acc atc gcc cgc gac tac tgg aat aac ggt atc cgc 336
Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg
100 105 110
cac att gtc gct ttg cgc ggc gat ttg ccg ccg ggc agc ggt aag ccg 384
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
115 120 125
gag atg tac gcc gcc gat ctg gtt ggt ttg ctc aaa gag gtg gcc gat 432
Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Ala Asp
130 135 140
ttc gat att tca gta gcg gcc tat ccg gag gta cat ccg gaa gcg aaa 480
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
145 150 155 160
agc gcg cag gcc gat ctg ctt aat ctg aag cgt aaa gtg gat gct ggc 528
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly
165 170 175
gct aac cgc gcg ata acc caa ttt ttc ttc gat gtg gaa agc tac ctg 576

Ala	Asn	Arg	Ala	Ile	Thr	Gln	Phe	Phe	Phe	Asp	Val	Glu	Ser	Tyr	Leu	
			180					185					190			
cgt	ttt	cgc	gac	cgc	tgt	gtt	tct	gcc	ggg	atc	gac	gta	gaa	att	att	624
Arg	Phe	Arg	Asp	Arg	Cys	Val	Ser	Ala	Gly	Ile	Asp	Val	Glu	Ile	Ile	
		195					200					205				
ccc	ggc	att	tta	ccg	gtg	tct	aac	ttt	aaa	cag	gca	aaa	aaa	ttt	gcc	672
Pro	Gly	Ile	Leu	Pro	Val	Ser	Asn	Phe	Lys	Gln	Ala	Lys	Lys	Phe	Ala	
	210					215				220						
gat	atg	acc	aat	gtc	cgc	att	ccg	tcc	tgg	atg	tca	ctg	atg	ttt	gag	720
Asp	Met	Thr	Asn	Val	Arg	Ile	Pro	Ser	Trp	Met	Ser	Leu	Met	Phe	Glu	
225					230				235						240	
ggg	ctg	gat	aat	gac	gca	gaa	acc	cgc	aag	ctg	gtg	ggc	gct	aac	att	768
Gly	Leu	Asp	Asn	Asp	Ala	Glu	Thr	Arg	Lys	Leu	Val	Gly	Ala	Asn	Ile	
				245					250					255		
gcg	atg	gac	atg	gtg	aaa	att	tta	agc	cgt	gaa	gga	gtg	aag	gat	ttc	816
Ala	Met	Asp	Met	Val	Lys	Ile	Leu	Ser	Arg	Glu	Gly	Val	Lys	Asp	Phe	
			260					265					270			
cac	ttc	tac	acg	ttg	aat	cgt	gcg	gaa	atg	agt	tat	gcc	att	tgc	cac	864
His	Phe	Tyr	Thr	Leu	Asn	Arg	Ala	Glu	Met	Ser	Tyr	Ala	Ile	Cys	His	
		275					280					285				
acg	ctg	ggc	gta	aga	ccg	ggg	tta	taa								891
Thr	Leu	Gly	Val	Arg	Pro	Gly	Leu									
	290					295										

<210> 32
 <211> 296
 <212> PRT
 <213> Salmonella typhimurium

<400> 32
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 20 25 30
 Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
 35 40 45
 Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60
 Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg
 65 70 75 80
 Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg
 85 90 95
 Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg
 100 105 110
 His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
 115 120 125

Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Ala Asp
 130 135 140
 Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145 150 155 160
 Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly
 165 170 175
 Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
 180 185 190
 Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile
 195 200 205
 Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
 210 215 220
 Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu
 225 230 235 240
 Gly Leu Asp Asn Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile
 245 250 255
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270
 His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
 275 280 285
 Thr Leu Gly Val Arg Pro Gly Leu
 290 295

<210> 33
 <211> 891
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(888)
 <223> REC03839

<400> 33
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 gca gaa gtc cag ggg cag att aac gtt tcg ttc gag ttt ttc ccg ccg 96
 Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30
 cgt acc agt gaa atg gag cag acc ctg tgg aac tcc atc gat cgc ctt 144
 Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
 35 40 45
 agc agc ctg aaa ccg aag ttt gta tcg gtg acc tat ggc gcg aac tcc 192
 Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser

50	55	60	
ggc gag cgc gac cgt acg cac agc att att aaa ggc att aaa gat cgc Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Asp Arg 65 70 75 80			240
act ggt ctg gaa gcg gca ccg cat ctt act tgc att gat gcg acg ccc Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Pro 85 90 95			288
gac gag ctg cgc acc att gca cgc gac tac tgg aat aac ggt att cgt Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg 100 105 110			336
cat atc gtg gcg ctg cgt ggc gat ctg ccg ccg gga agt ggt aag cca His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro 115 120 125			384
gaa atg tat gct tct gac ctg gtg acg ctg tta aaa gaa gtg gca gat Glu Met Tyr Ala Ser Asp Leu Val Thr Leu Leu Lys Glu Val Ala Asp 130 135 140			432
ttc gat atc tcc gtg gcg gcg tat ccg gaa gtt cac ccg gaa gca aaa Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys 145 150 155 160			480
agc gct cag gcg gat ttg ctt aat ctg aaa cgc aaa gtg gat gcc gga Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly 165 170 175			528
gcc aac cgc gcg att act cag ttc ttc ttc gat gtc gaa agc tac ctg Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu 180 185 190			576
cgt ttt cgt gac cgc tgt gta tcg gcg ggc att gat gtg gaa att att Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile 195 200 205			624
ccg gga att ttg ccg gta tct aac ttt aaa cag gcg aag aaa ttt gcc Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala 210 215 220			672
gat atg acc aac gtg cgt att ccg gcg tgg atg gcg caa atg ttc gac Asp Met Thr Asn Val Arg Ile Pro Ala Trp Met Ala Gln Met Phe Asp 225 230 235 240			720
ggt ctg gat gat gat gcc gaa acc cgc aaa ctg gtt ggc gcg aat att Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile 245 250 255			768
gcc atg gat atg gtg aag att tta agc cgt gaa gga gtg aaa gat ttc Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe 260 265 270			816
cac ttc tat acg ctt aac cgt gct gaa atg agt tac gcg att tgc cat His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His 275 280 285			864
acg ctg ggg gtt cga cct ggt tta taa Thr Leu Gly Val Arg Pro Gly Leu 290 295			891

<210> 34
 <211> 296
 <212> PRT
 <213> Escherichia coli

<400> 34

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Met Ser Phe Phe His Ala Ser Gln Arg Asp Ala Leu Asn Gln Ser Leu
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      20             25             30

Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
      35             40             45

Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50             55             60

Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Asp Arg
 65             70             75             80

Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Pro
      85             90             95

Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg
      100             105             110

His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
      115             120             125

Glu Met Tyr Ala Ser Asp Leu Val Thr Leu Leu Lys Glu Val Ala Asp
 130             135             140

Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145             150             155             160

Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly
      165             170             175

Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
      180             185             190

Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile
      195             200             205

Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
 210             215             220

Asp Met Thr Asn Val Arg Ile Pro Ala Trp Met Ala Gln Met Phe Asp
 225             230             235             240

Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile
      245             250             255

Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
      260             265             270

His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
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Thr Leu Gly Val Arg Pro Gly Leu
290 295

<210> 35
<211> 915
<212> DNA
<213> *Vibrio cholerae*

<220>
<221> CDS
<222> (1)..(912)
<223> RVC06433

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cat atc gat gca ttg aac caa aac att gcg gag ctt tcc gac atc aat 96
His Ile Asp Ala Leu Asn Gln Asn Ile Ala Glu Leu Ser Asp Ile Asn
20 25 30

gtt tcg ttt gag ttt ttt cca ccc agc tca cca caa atg gaa gaa acg 144
Val Ser Phe Glu Phe Phe Pro Pro Ser Ser Pro Gln Met Glu Glu Thr
35 40 45

ctt tgg gga tcg gta cac cgt ctg aaa aca ctc caa ccg aaa ttt gtt 192
Leu Trp Gly Ser Val His Arg Leu Lys Thr Leu Gln Pro Lys Phe Val
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tcg gtc act tat ggt gca aac tct ggt gag cgt gac cgt act cac tcg 240
Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu Arg Asp Arg Thr His Ser
65 70 75 80

atc att aaa gcg atc aaa gat caa acc ggt tta att gcc gcg cca cac 288
Ile Ile Lys Ala Ile Lys Asp Gln Thr Gly Leu Ile Ala Ala Pro His
85 90 95

ctg act tgt atc gat gcc act cgt gat gaa ctg atc cag atc gcc gat 336
Leu Thr Cys Ile Asp Ala Thr Arg Asp Glu Leu Ile Gln Ile Ala Asp
100 105 110

gac tac tgg cat aac ggc atc cag aat att gtg gcg ctg cgt ggg gat 384
Asp Tyr Trp His Asn Gly Ile Gln Asn Ile Val Ala Leu Arg Gly Asp
115 120 125

atc ccg gct ggc ggt ggt aag cca gag atg tac gcc tcc gat cta gtg 432
Ile Pro Ala Gly Gly Gly Lys Pro Glu Met Tyr Ala Ser Asp Leu Val
130 135 140

acg ctg ctc aaa tca cgc cac gat ttt gat att tcc gtg gcc gcc ttc 480
Thr Leu Leu Lys Ser Arg His Asp Phe Asp Ile Ser Val Ala Ala Phe
145 150 155 160

cct gaa gtg cac cct gaa gcc aaa agc gcg caa gcg gac ctg ctc aat 528
Pro Glu Val His Pro Glu Ala Lys Ser Ala Gln Ala Asp Leu Leu Asn
165 170 175

tta aaa cgt aaa gtc gat gca ggt gcg aat cgt gcc atc acg cag ttt 576

Leu	Lys	Arg	Lys	Val	Asp	Ala	Gly	Ala	Asn	Arg	Ala	Ile	Thr	Gln	Phe		
			180					185					190				
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Phe	Phe	Asp	Val	Glu	Ser	Tyr	Leu	Arg	Phe	Arg	Asp	Arg	Cys	Val	Ala		
		195					200				205						
gct	ggg	att	gac	gta	gaa	atc	gtg	cct	ggc	att	ctg	ccg	ggt	tct	aac	672	
Ala	Gly	Ile	Asp	Val	Glu	Ile	Val	Pro	Gly	Ile	Leu	Pro	Val	Ser	Asn		
	210					215					220						
ttt	aaa	caa	gcg	tcg	cgc	ttc	gct	gcg	caa	aac	aac	gtc	aaa	ggt	ccg	720	
Phe	Lys	Gln	Ala	Ser	Arg	Phe	Ala	Ala	Gln	Asn	Asn	Val	Lys	Val	Pro		
225					230					235					240		
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Asn	Trp	Met	Val	Lys	Gln	Phe	Glu	Gly	Leu	Glu	Asp	Asp	Pro	Val	Thr		
			245						250					255			
cgc	cag	ttg	gta	ggg	gca	agc	caa	gcc	att	gat	atg	gtg	cgc	gtg	ctg	816	
Arg	Gln	Leu	Val	Gly	Ala	Ser	Gln	Ala	Ile	Asp	Met	Val	Arg	Val	Leu		
			260					265					270				
tgc	cgt	gaa	ggg	gtg	aag	gat	ttc	cac	ttc	tac	acc	cta	aat	cgt	gcc	864	
Cys	Arg	Glu	Gly	Val	Lys	Asp	Phe	His	Phe	Tyr	Thr	Leu	Asn	Arg	Ala		
		275					280					285					
gaa	atg	act	tac	gcg	tta	tgc	cac	acc	tta	ggc	ggt	cgc	cca	caa	gct	912	
Glu	Met	Thr	Tyr	Ala	Leu	Cys	His	Thr	Leu	Gly	Val	Arg	Pro	Gln	Ala		
	290					295					300						
taa																915	

<210> 36
 <211> 304
 <212> PRT
 <213> *Vibrio cholerae*

<400> 36
 Val Thr Leu Gly His Arg Glu Tyr Lys Met Gly Tyr Thr His Ala Ser
 1 5 10 15
 His Ile Asp Ala Leu Asn Gln Asn Ile Ala Glu Leu Ser Asp Ile Asn
 20 25 30
 Val Ser Phe Glu Phe Phe Pro Pro Ser Ser Pro Gln Met Glu Glu Thr
 35 40 45
 Leu Trp Gly Ser Val His Arg Leu Lys Thr Leu Gln Pro Lys Phe Val
 50 55 60
 Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu Arg Asp Arg Thr His Ser
 65 70 75 80
 Ile Ile Lys Ala Ile Lys Asp Gln Thr Gly Leu Ile Ala Ala Pro His
 85 90 95
 Leu Thr Cys Ile Asp Ala Thr Arg Asp Glu Leu Ile Gln Ile Ala Asp
 100 105 110

Asp Tyr Trp His Asn Gly Ile Gln Asn Ile Val Ala Leu Arg Gly Asp
 115 120 125
 Ile Pro Ala Gly Gly Gly Lys Pro Glu Met Tyr Ala Ser Asp Leu Val
 130 135 140
 Thr Leu Leu Lys Ser Arg His Asp Phe Asp Ile Ser Val Ala Ala Phe
 145 150 155 160
 Pro Glu Val His Pro Glu Ala Lys Ser Ala Gln Ala Asp Leu Leu Asn
 165 170 175
 Leu Lys Arg Lys Val Asp Ala Gly Ala Asn Arg Ala Ile Thr Gln Phe
 180 185 190
 Phe Phe Asp Val Glu Ser Tyr Leu Arg Phe Arg Asp Arg Cys Val Ala
 195 200 205
 Ala Gly Ile Asp Val Glu Ile Val Pro Gly Ile Leu Pro Val Ser Asn
 210 215 220
 Phe Lys Gln Ala Ser Arg Phe Ala Ala Gln Asn Asn Val Lys Val Pro
 225 230 235 240
 Asn Trp Met Val Lys Gln Phe Glu Gly Leu Glu Asp Asp Pro Val Thr
 245 250 255
 Arg Gln Leu Val Gly Ala Ser Gln Ala Ile Asp Met Val Arg Val Leu
 260 265 270
 Cys Arg Glu Gly Val Lys Asp Phe His Phe Tyr Thr Leu Asn Arg Ala
 275 280 285
 Glu Met Thr Tyr Ala Leu Cys His Thr Leu Gly Val Arg Pro Gln Ala
 290 295 300

<210> 37
 <211> 879
 <212> DNA
 <213> Haemophilus influenzae

<220>
 <221> CDS
 <222> (1)..(876)
 <223> RHI06620

<400> 37
 atg agc tac gcg aaa gaa att gat aca tta aat caa cat att gca gat 48
 Met Ser Tyr Ala Lys Glu Ile Asp Thr Leu Asn Gln His Ile Ala Asp
 1 5 10 15
 ttt aat aaa aaa att aat gtc tcc ttt gaa ttt ttt cca cct aaa aac 96
 Phe Asn Lys Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn
 20 25 30
 gaa aaa atg gaa acc ctt cta tgg gat tca att cat cgt tta aaa gta 144
 Glu Lys Met Glu Thr Leu Leu Trp Asp Ser Ile His Arg Leu Lys Val

35	40	45	
tta aag cct aaa ttt gtg tca gtc act tac ggt gca aat tcg gga gaa Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu 50 55 60			192
cgt gac cgc act cac ggc att gtg aaa gcc att aaa caa gaa act ggc Arg Asp Arg Thr His Gly Ile Val Lys Ala Ile Lys Gln Glu Thr Gly 65 70 75 80			240
tta gaa gcc gca cca cat tta act gga att gat gcc aca cct gaa gaa Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Pro Glu Glu 85 90 95			288
tta aaa caa att gcg aga gat tat tgg gat agt ggt att cgc cgt att Leu Lys Gln Ile Ala Arg Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile 100 105 110			336
gtt gcg tta cgc ggt gac gaa cct aaa ggt tac gcg aaa aaa cca ttt Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Ala Lys Lys Pro Phe 115 120 125			384
tat gcg tca gat ctt gtg gaa tta ctc cgt tct gtc gct gat ttt gat Tyr Ala Ser Asp Leu Val Glu Leu Leu Arg Ser Val Ala Asp Phe Asp 130 135 140			432
att tct gta gcc gct tat ccc gaa gtt cat cca gaa gca aaa tcc gca Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala 145 150 155 160			480
caa gca gac tta att aat tta aaa cgt aaa att gat gca ggt gca aac Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn 165 170 175			528
cac gtc att aca caa ttt ttc ttt gat att gaa aac tac cta cgt ttt His Val Ile Thr Gln Phe Phe Phe Asp Ile Glu Asn Tyr Leu Arg Phe 180 185 190			576
cgt gat cgt tgt gca tca att ggt att gat act gaa atc gta ccc ggt Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Thr Glu Ile Val Pro Gly 195 200 205			624
att tta cct gtt act aat ttt aaa caa ctc caa aaa atg gca tca ttc Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ser Phe 210 215 220			672
act aat gtg aaa att cca gcg tgg tta gtt aaa gcc tat gat ggt ttg Thr Asn Val Lys Ile Pro Ala Trp Leu Val Lys Ala Tyr Asp Gly Leu 225 230 235 240			720
gat aat gat cca act aca cgt aat ctt gtg gca gca agt gtt gca atg Asp Asn Asp Pro Thr Thr Arg Asn Leu Val Ala Ala Ser Val Ala Met 245 250 255			768
gat atg gta aaa att tta tct cgc gaa ggc gtg aat gac ttc cac ttt Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Asn Asp Phe His Phe 260 265 270			816
tat aca tta aat cgt agt gaa tta act tat gct atc tgt cat atg tta Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Met Leu 275 280 285			864

ggt gta aga cct taa
Gly Val Arg Pro
290

879

<210> 38
<211> 292
<212> PRT
<213> Haemophilus influenzae

<400> 38
Met Ser Tyr Ala Lys Glu Ile Asp Thr Leu Asn Gln His Ile Ala Asp
1 5 10 15

Phe Asn Lys Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn
20 25 30

Glu Lys Met Glu Thr Leu Leu Trp Asp Ser Ile His Arg Leu Lys Val
35 40 45

Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu
50 55 60

Arg Asp Arg Thr His Gly Ile Val Lys Ala Ile Lys Gln Glu Thr Gly
65 70 75 80

Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Pro Glu Glu
85 90 95

Leu Lys Gln Ile Ala Arg Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile
100 105 110

Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Ala Lys Lys Pro Phe
115 120 125

Tyr Ala Ser Asp Leu Val Glu Leu Leu Arg Ser Val Ala Asp Phe Asp
130 135 140

Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala
145 150 155 160

Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn
165 170 175

His Val Ile Thr Gln Phe Phe Phe Asp Ile Glu Asn Tyr Leu Arg Phe
180 185 190

Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Thr Glu Ile Val Pro Gly
195 200 205

Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ser Phe
210 215 220

Thr Asn Val Lys Ile Pro Ala Trp Leu Val Lys Ala Tyr Asp Gly Leu
225 230 235 240

Asp Asn Asp Pro Thr Thr Arg Asn Leu Val Ala Ala Ser Val Ala Met
245 250 255

Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Asn Asp Phe His Phe
 260 265 270

Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Met Leu
 275 280 285

Gly Val Arg Pro
 290

<210> 39
 <211> 945
 <212> DNA
 <213> *Caulobacter crescentus*

<220>
 <221> CDS
 <222> (1)..(942)
 <223> RCO02274

<400> 39
 atg acc ctt ccg ccc acc cgc cgc gtg atc ggt ccc gtc gcc cga gcc 48
 Met Thr Leu Pro Pro Thr Arg Arg Val Ile Gly Pro Val Ala Arg Ala
 1 5 10 15
 ggc gag cgg acc ggc cgt ccg cgc gtg tcg ttc gag ttc ttc ccg ccc 96
 Gly Glu Arg Thr Gly Arg Pro Arg Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30
 aag act ccg cag atg gaa gag agc ctg tgg cag gcg atc aca cgc ctg 144
 Lys Thr Pro Gln Met Glu Glu Ser Leu Trp Gln Ala Ile Thr Arg Leu
 35 40 45
 gcg ccg ctg gat ccg gcc ttc gtc tcg gtg acc tat ggc gcg ggc ggc 192
 Ala Pro Leu Asp Pro Ala Phe Val Ser Val Thr Tyr Gly Ala Gly Gly
 50 55 60
 tcc acc cgc gag cgc acc cac cgc acc gtc aag cgg atc ctg gac gag 240
 Ser Thr Arg Glu Arg Thr His Arg Thr Val Lys Arg Ile Leu Asp Glu
 65 70 75 80
 acc agc ctc aag ccc gcc gcg cac ctg acc tgc gtc ggc gcc agt cgc 288
 Thr Ser Leu Lys Pro Ala Ala His Leu Thr Cys Val Gly Ala Ser Arg
 85 90 95
 gaa gag gtc gat gag gtc att cgc gag tac tgg gag acc ggg gtc cgt 336
 Glu Glu Val Asp Glu Val Ile Arg Glu Tyr Trp Glu Thr Gly Val Arg
 100 105 110
 cac atc gtt tcg ctg cgg ggc gat ccg ccg ccc ggc gag ggc ggc atc 384
 His Ile Val Ser Leu Arg Gly Asp Pro Pro Pro Gly Glu Gly Gly Ile
 115 120 125
 ggc ggg gtc tat gtg ccg cgc gcc gac ggc tac gcc aac gcc aca gag 432
 Gly Gly Val Tyr Val Pro Arg Ala Asp Gly Tyr Ala Asn Ala Thr Glu
 130 135 140
 ttg acc aag gcc gtg cgc gcg atc gcg ccg ttc gag gtg ctg gtc ggg 480
 Leu Thr Lys Ala Val Arg Ala Ile Ala Pro Phe Glu Val Leu Val Gly
 145 150 155 160

gtc tat ccc gag aag cat ccc gag agc ccc tcg ttg gag cac gac atc 528
 Val Tyr Pro Glu Lys His Pro Glu Ser Pro Ser Leu Glu His Asp Ile
 165 170 175

gac gtc ttg aag cag aag gtc gac gcc gcc ggc acg ctg ggg atc agc 576
 Asp Val Leu Lys Gln Lys Val Asp Ala Gly Ala Thr Leu Gly Ile Ser
 180 185 190

cag ttc ttc ttc gac ctc gac gcc ttc ctg cgc ttc gtc gac aag gtg 624
 Gln Phe Phe Phe Asp Leu Asp Ala Phe Leu Arg Phe Val Asp Lys Val
 195 200 205

cgc gcg gcg gcc atc acc att ccg atc gtg ccg ggg atc atg ccg gtg 672
 Arg Ala Ala Gly Ile Thr Ile Pro Ile Val Pro Gly Ile Met Pro Val
 210 215 220

acc aat ttc gcg gcc ttg aag aag atg gcc gcc gcc tgc cag acg gcc 720
 Thr Asn Phe Ala Gly Leu Lys Lys Met Ala Ala Ala Cys Gln Thr Ala
 225 230 235 240

atc ccg tcc tgg ctg ggg aac ctg ttc gac ggg ctg gag aac gac gcg 768
 Ile Pro Ser Trp Leu Gly Asn Leu Phe Asp Gly Leu Glu Asn Asp Ala
 245 250 255

gag acc cgc cgc ctg atc gcc tgt tcg gtg gcc gcc gag atg tgc gcc 816
 Glu Thr Arg Arg Leu Ile Ala Cys Ser Val Ala Ala Glu Met Cys Ala
 260 265 270

aag ctg cag gaa cag ggt ttc gag gac ttc cac ttc tac acc ctg aac 864
 Lys Leu Gln Glu Gln Gly Phe Glu Asp Phe His Phe Tyr Thr Leu Asn
 275 280 285

cgg gcc gat ctc gtt tac gcc atc tgc cgt gtg ctg gcc gtg cgc gag 912
 Arg Ala Asp Leu Val Tyr Ala Ile Cys Arg Val Leu Gly Val Arg Glu
 290 295 300

atc tcg ccc gcc gct tcg gag gtc gcc gca tga 945
 Ile Ser Pro Ala Ala Ser Glu Val Ala Ala
 305 310

<210> 40
 <211> 314
 <212> PRT
 <213> *Caulobacter crescentus*

<400> 40
 Met Thr Leu Pro Pro Thr Arg Arg Val Ile Gly Pro Val Ala Arg Ala
 1 5 10 15

Gly Glu Arg Thr Gly Arg Pro Arg Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30

Lys Thr Pro Gln Met Glu Glu Ser Leu Trp Gln Ala Ile Thr Arg Leu
 35 40 45

Ala Pro Leu Asp Pro Ala Phe Val Ser Val Thr Tyr Gly Ala Gly Gly
 50 55 60

Ser Thr Arg Glu Arg Thr His Arg Thr Val Lys Arg Ile Leu Asp Glu
 65 70 75 80

Thr Ser Leu Lys Pro Ala Ala His Leu Thr Cys Val Gly Ala Ser Arg
 85 90 95
 Glu Glu Val Asp Glu Val Ile Arg Glu Tyr Trp Glu Thr Gly Val Arg
 100 105 110
 His Ile Val Ser Leu Arg Gly Asp Pro Pro Pro Gly Glu Gly Gly Ile
 115 120 125
 Gly Gly Val Tyr Val Pro Arg Ala Asp Gly Tyr Ala Asn Ala Thr Glu
 130 135 140
 Leu Thr Lys Ala Val Arg Ala Ile Ala Pro Phe Glu Val Leu Val Gly
 145 150 155 160
 Val Tyr Pro Glu Lys His Pro Glu Ser Pro Ser Leu Glu His Asp Ile
 165 170 175
 Asp Val Leu Lys Gln Lys Val Asp Ala Gly Ala Thr Leu Gly Ile Ser
 180 185 190
 Gln Phe Phe Phe Asp Leu Asp Ala Phe Leu Arg Phe Val Asp Lys Val
 195 200 205
 Arg Ala Ala Gly Ile Thr Ile Pro Ile Val Pro Gly Ile Met Pro Val
 210 215 220
 Thr Asn Phe Ala Gly Leu Lys Lys Met Ala Ala Ala Cys Gln Thr Ala
 225 230 235 240
 Ile Pro Ser Trp Leu Gly Asn Leu Phe Asp Gly Leu Glu Asn Asp Ala
 245 250 255
 Glu Thr Arg Arg Leu Ile Ala Cys Ser Val Ala Ala Glu Met Cys Ala
 260 265 270
 Lys Leu Gln Glu Gln Gly Phe Glu Asp Phe His Phe Tyr Thr Leu Asn
 275 280 285
 Arg Ala Asp Leu Val Tyr Ala Ile Cys Arg Val Leu Gly Val Arg Glu
 290 295 300
 Ile Ser Pro Ala Ala Ser Glu Val Ala Ala
 305 310

<210> 41
 <211> 885
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(882)

<223> RAB00260

<400> 41
 atg agt tac gca aaa gaa att gat aat cta aat caa cat tta gct gat
 Met Ser Tyr Ala Lys Glu Ile Asp Asn Leu Asn Gln His Leu Ala Asp

48

1	5	10	15	
tta aac ggc aaa att aat gtc tct ttt gaa ttt ttc ccg ccg aaa agt				96
Leu Asn Gly Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Ser	20	25	30	
gaa aaa atg gaa aat ctt ctg tgg gaa tcc atc cat cgc tta aaa gtg				144
Glu Lys Met Glu Asn Leu Leu Trp Glu Ser Ile His Arg Leu Lys Val	35	40	45	
cta aaa ccg aaa ttt gta tcc gtg act tac ggc gcc aat tcc ggc gag				192
Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu	50	55	60	
cgt gaa cgc act cac ggg gtg gtg aaa cgc att aag cag gaa acc ggt				240
Arg Glu Arg Thr His Gly Val Val Lys Arg Ile Lys Gln Glu Thr Gly	65	70	75	80
ctg gaa gct gcg ccg cat tta acc ggt att gac gct acc tcg gac gaa				288
Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Ser Asp Glu	85	90	95	
ttg cgt cgc att gcc aaa ggt tat tgg gat agc ggc att cgt cgc att				336
Leu Arg Arg Ile Ala Lys Gly Tyr Trp Asp Ser Gly Ile Arg Arg Ile	100	105	110	
gtg gca ctg cgc ggt gac gag ccg aaa ggc tac gag aaa aaa cca ttt				384
Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Glu Lys Lys Pro Phe	115	120	125	
tat gcc gcc gat tta gta gca tta tta cgt gac gta tca gat ttt gat				432
Tyr Ala Ala Asp Leu Val Ala Leu Leu Arg Asp Val Ser Asp Phe Asp	130	135	140	
att tcc gtg gcg gca tac cct gag gtt cat ccg gaa gcc aaa tcg gcg				480
Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala	145	150	155	160
caa gcg gat tta att aat tta aaa cgt aaa att gat gcc ggt gcc aat				528
Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn	165	170	175	
cat gtg atc aca caa ttc ttt ttc gat att gac agc tat ctg cgg ttc				576
His Val Ile Thr Gln Phe Phe Phe Asp Ile Asp Ser Tyr Leu Arg Phe	180	185	190	
cgc gat cgc tgc gcg tct atc ggt att gat gca gaa atc gtg ccg ggg				624
Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Ala Glu Ile Val Pro Gly	195	200	205	
att ctg ccg gtg acc aac ttc aaa caa tta caa aaa atg gca gca atc				672
Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ala Ile	210	215	220	
act aat gtg aaa att cca gct tgg atg agc aaa atg tat gaa ggc ttg				720
Thr Asn Val Lys Ile Pro Ala Trp Met Ser Lys Met Tyr Glu Gly Leu	225	230	235	240
gat gat gac caa acc acc cgc aat ctg gtg gcg gcg agc atc gcc atg				768
Asp Asp Asp Gln Thr Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Met	245	250	255	

gac atg gtg cgt gta ctg tcc cgc gaa ggg gta aaa gac ttt cat ttc 816
 Asp Met Val Arg Val Leu Ser Arg Glu Gly Val Lys Asp Phe His Phe
 260 265 270

tac acc ctg aat cgc agt gaa ctc acc tat gct att tgc cac acg tta 864
 Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Thr Leu
 275 280 285

ggc att cgt ccg agt ttg taa 885
 Gly Ile Arg Pro Ser Leu
 290

<210> 42

<211> 294

<212> PRT

<213> Actinobacillus actinomycetemcomitans

<400> 42

Met Ser Tyr Ala Lys Glu Ile Asp Asn Leu Asn Gln His Leu Ala Asp
 1 5 10 15

Leu Asn Gly Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Ser
 20 25 30

Glu Lys Met Glu Asn Leu Leu Trp Glu Ser Ile His Arg Leu Lys Val
 35 40 45

Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu
 50 55 60

Arg Glu Arg Thr His Gly Val Val Lys Arg Ile Lys Gln Glu Thr Gly
 65 70 75 80

Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Ser Asp Glu
 85 90 95

Leu Arg Arg Ile Ala Lys Gly Tyr Trp Asp Ser Gly Ile Arg Arg Ile
 100 105 110

Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Glu Lys Lys Pro Phe
 115 120 125

Tyr Ala Ala Asp Leu Val Ala Leu Leu Arg Asp Val Ser Asp Phe Asp
 130 135 140

Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala
 145 150 155 160

Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn
 165 170 175

His Val Ile Thr Gln Phe Phe Phe Asp Ile Asp Ser Tyr Leu Arg Phe
 180 185 190

Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Ala Glu Ile Val Pro Gly
 195 200 205

Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ala Ile
 210 215 220

Thr Asn Val Lys Ile Pro Ala Trp Met Ser Lys Met Tyr Glu Gly Leu
 225 230 235 240
 Asp Asp Asp Gln Thr Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Met
 245 250 255
 Asp Met Val Arg Val Leu Ser Arg Glu Gly Val Lys Asp Phe His Phe
 260 265 270
 Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Thr Leu
 275 280 285
 Gly Ile Arg Pro Ser Leu
 290

<210> 43
 <211> 867
 <212> DNA
 <213> Rhodobacter

<220>
 <221> CDS
 <222> (1)..(864)
 <223> RRC03981

<400> 43
 atg acc acg ccg cat gtc agc ttt gaa ttc ttc ccg ccg cag acg ctc 48
 Met Thr Thr Pro His Val Ser Phe Glu Phe Phe Pro Pro Gln Thr Leu
 1 5 10 15
 gac gcc tcg ttc ccg ctg tgg gag acg gcg cag gtt ctg gcg ccg ctc 96
 Asp Ala Ser Phe Arg Leu Trp Glu Thr Ala Gln Val Leu Ala Pro Leu
 20 25 30
 aag ccc ggc ttc gtc tcg gtc acc tat ggc gcg ggc ggc acc acc cgc 144
 Lys Pro Gly Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Thr Thr Arg
 35 40 45
 aag ctg acg cat gag gcc gtg gcg gcg atc cac aag aat tac ggc ctg 192
 Lys Leu Thr His Glu Ala Val Ala Ala Ile His Lys Asn Tyr Gly Leu
 50 55 60
 aac gtc gcc gcg cat ctg acc tgc gtc gat gcg acc ccg gcc gaa acg 240
 Asn Val Ala Ala His Leu Thr Cys Val Asp Ala Thr Arg Ala Glu Thr
 65 70 75 80
 caa gag atc atc gac gcc tat gcc gag gct ggc gtc acc gag att gtc 288
 Gln Glu Ile Ile Asp Ala Tyr Ala Glu Ala Gly Val Thr Glu Ile Val
 85 90 95
 gcg ctg cgc ggt gat ccg ccg aaa ggc gcc gcc cgc ttc acg ccg cat 336
 Ala Leu Arg Gly Asp Pro Pro Lys Gly Ala Ala Arg Phe Thr Pro His
 100 105 110
 ccg gac ggg ttt gcc tcc tcg gtg gac ctc atc gaa tgg ctg gcg ccg 384
 Pro Asp Gly Phe Ala Ser Ser Val Asp Leu Ile Glu Trp Leu Ala Arg
 115 120 125
 gac ggc cgc ttc acg ctg cgc tgc ggc gcc tat ccg gaa ccg cat ccg 432

Asp	Gly	Arg	Phe	Thr	Leu	Arg	Cys	Gly	Ala	Tyr	Pro	Glu	Pro	His	Pro		
130						135					140						
gaa	gcc	gcc	gac	acg	ctg	gcc	gac	gtg	cgc	tgg	ctg	aaa	cgc	aaa	tgc	480	
Glu	Ala	Ala	Asp	Thr	Leu	Ala	Asp	Val	Arg	Trp	Leu	Lys	Arg	Lys	Cys		
145					150				155						160		
gag	gcg	ggg	gcg	acc	tgc	gcg	atc	acg	caa	ttc	ttc	ttt	gaa	gcc	gag	528	
Glu	Ala	Gly	Ala	Thr	Ser	Ala	Ile	Thr	Gln	Phe	Phe	Phe	Glu	Ala	Glu		
				165					170					175			
acc	ttc	ttc	cgc	ttc	cgc	gac	gcc	tgc	gtg	aag	gaa	ggg	atc	acc	gcc	576	
Thr	Phe	Phe	Arg	Phe	Arg	Asp	Ala	Cys	Val	Lys	Glu	Gly	Ile	Thr	Ala		
			180					185					190				
aag	atc	atc	ccg	ggc	atc	ctg	ccg	atc	cag	tcc	tgg	aaa	ggc	gcc	aag	624	
Lys	Ile	Ile	Pro	Gly	Ile	Leu	Pro	Ile	Gln	Ser	Trp	Lys	Gly	Ala	Lys		
		195					200					205					
agc	ttt	gcg	cag	cgc	tgc	ggc	acc	tgc	atc	ccg	acc	tgg	gtc	gaa	gag	672	
Ser	Phe	Ala	Gln	Arg	Cys	Gly	Thr	Ser	Ile	Pro	Thr	Trp	Val	Glu	Glu		
	210					215					220						
gcc	ttt	gac	cat	gcg	atc	cgc	gac	gac	cgc	gaa	cag	ctg	ctg	gcc	acg	720	
Ala	Phe	Asp	His	Ala	Ile	Arg	Asp	Asp	Arg	Glu	Gln	Leu	Leu	Ala	Thr		
225					230				235						240		
gcg	ctg	tgc	acg	gag	ctc	tgc	gac	aac	ctg	atc	gcg	ggc	ggg	gtg	gag	768	
Ala	Leu	Cys	Thr	Glu	Leu	Cys	Asp	Asn	Leu	Ile	Ala	Gly	Gly	Val	Glu		
				245					250					255			
gat	ctg	cat	ttc	tac	acg	ctg	aac	cgg	ccg	cag	atg	acc	cgc	gat	gtc	816	
Asp	Leu	His	Phe	Tyr	Thr	Leu	Asn	Arg	Pro	Gln	Met	Thr	Arg	Asp	Val		
			260					265					270				
tgc	cat	gcg	ctg	ggc	gtc	aac	ccg	ggt	gtg	gtg	ctg	gaa	aac	gtc	gcc	864	
Cys	His	Ala	Leu	Gly	Val	Asn	Pro	Gly	Val	Val	Leu	Glu	Asn	Val	Ala		
		275					280					285					
tga																867	

<210> 44
 <211> 288
 <212> PRT
 <213> Rhodobacter

<400> 44
 Met Thr Thr Pro His Val Ser Phe Glu Phe Phe Pro Pro Gln Thr Leu
 1 5 10 15
 Asp Ala Ser Phe Arg Leu Trp Glu Thr Ala Gln Val Leu Ala Pro Leu
 20 25 30
 Lys Pro Gly Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Thr Thr Arg
 35 40 45
 Lys Leu Thr His Glu Ala Val Ala Ala Ile His Lys Asn Tyr Gly Leu
 50 55 60
 Asn Val Ala Ala His Leu Thr Cys Val Asp Ala Thr Arg Ala Glu Thr

65	70	75	80
Gln Glu Ile Ile Asp Ala Tyr Ala Glu Ala Gly Val Thr Glu Ile Val	85	90	95
Ala Leu Arg Gly Asp Pro Pro Lys Gly Ala Ala Arg Phe Thr Pro His	100	105	110
Pro Asp Gly Phe Ala Ser Ser Val Asp Leu Ile Glu Trp Leu Ala Arg	115	120	125
Asp Gly Arg Phe Thr Leu Arg Cys Gly Ala Tyr Pro Glu Pro His Pro	130	135	140
Glu Ala Ala Asp Thr Leu Ala Asp Val Arg Trp Leu Lys Arg Lys Cys	145	150	155
Glu Ala Gly Ala Thr Ser Ala Ile Thr Gln Phe Phe Phe Glu Ala Glu	165	170	175
Thr Phe Phe Arg Phe Arg Asp Ala Cys Val Lys Glu Gly Ile Thr Ala	180	185	190
Lys Ile Ile Pro Gly Ile Leu Pro Ile Gln Ser Trp Lys Gly Ala Lys	195	200	205
Ser Phe Ala Gln Arg Cys Gly Thr Ser Ile Pro Thr Trp Val Glu Glu	210	215	220
Ala Phe Asp His Ala Ile Arg Asp Asp Arg Glu Gln Leu Leu Ala Thr	225	230	235
Ala Leu Cys Thr Glu Leu Cys Asp Asn Leu Ile Ala Gly Gly Val Glu	245	250	255
Asp Leu His Phe Tyr Thr Leu Asn Arg Pro Gln Met Thr Arg Asp Val	260	265	270
Cys His Ala Leu Gly Val Asn Pro Gly Val Val Leu Glu Asn Val Ala	275	280	285

<210> 45

<211> 879

<212> DNA

<213> Neisseria meningitidis ser. A

<220>

<221> CDS

<222> (1)..(876)

<223> RNM00812

<400> 45

atg aat tac gca aaa gaa atc aat gcg tta aat aac agc ctt tcc gat	48
Met Asn Tyr Ala Lys Glu Ile Asn Ala Leu Asn Asn Ser Leu Ser Asp	
1 5 10 15	

ttg aaa ggc gac atc aac gtt tcg ttt gaa ttt ttt cca ccg aaa aac	96
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Leu	Lys	Gly	Asp	Ile	Asn	Val	Ser	Phe	Glu	Phe	Phe	Pro	Pro	Lys	Asn	
			20					25					30			
gag	caa	atg	gaa	acg	atg	ctg	tgg	gat	tcc	atc	cac	cgt	ctg	caa	acc	144
Glu	Gln	Met	Glu	Thr	Met	Leu	Trp	Asp	Ser	Ile	His	Arg	Leu	Gln	Thr	
		35					40					45				
ctg	cat	ccc	aag	ttc	gta	tcc	gta	acc	tac	ggc	gca	aac	tcc	ggc	gaa	192
Leu	His	Pro	Lys	Phe	Val	Ser	Val	Thr	Tyr	Gly	Ala	Asn	Ser	Gly	Glu	
	50					55					60					
cgc	gac	cgc	acg	cac	ggc	atc	gtc	aaa	cgc	atc	aaa	cag	gaa	acc	ggc	240
Arg	Asp	Arg	Thr	His	Gly	Ile	Val	Lys	Arg	Ile	Lys	Gln	Glu	Thr	Gly	
65					70					75					80	
ttg	gaa	gca	gca	ccg	cac	ctg	acc	ggc	atc	gac	gca	tcc	ccc	gac	gaa	288
Leu	Glu	Ala	Ala	Pro	His	Leu	Thr	Gly	Ile	Asp	Ala	Ser	Pro	Asp	Glu	
				85					90					95		
ttg	cgc	caa	atc	gcc	aaa	gac	tat	tgg	gac	agc	ggc	atc	cgc	cgc	att	336
Leu	Arg	Gln	Ile	Ala	Lys	Asp	Tyr	Trp	Asp	Ser	Gly	Ile	Arg	Arg	Ile	
		100						105					110			
gtc	gcc	ctg	cgt	ggc	gac	gag	ccg	ccc	ggt	tat	gag	aaa	aaa	ccg	ttt	384
Val	Ala	Leu	Arg	Gly	Asp	Glu	Pro	Pro	Gly	Tyr	Glu	Lys	Lys	Pro	Phe	
		115					120					125				
tac	gcc	gaa	gac	ttg	gtt	aag	cta	tta	cgc	tcc	gtc	gcc	gac	ttc	gac	432
Tyr	Ala	Glu	Asp	Leu	Val	Lys	Leu	Leu	Arg	Ser	Val	Ala	Asp	Phe	Asp	
	130					135					140					
atc	tct	gtg	gcg	gca	tat	ccc	gaa	gtg	cat	ccc	gaa	gcc	aaa	tcc	gca	480
Ile	Ser	Val	Ala	Ala	Tyr	Pro	Glu	Val	His	Pro	Glu	Ala	Lys	Ser	Ala	
145					150					155					160	
caa	gcc	gat	ctg	att	aat	ctg	aag	cgc	aaa	atc	gat	gcg	ggt	gca	aac	528
Gln	Ala	Asp	Leu	Ile	Asn	Leu	Lys	Arg	Lys	Ile	Asp	Ala	Gly	Ala	Asn	
				165					170					175		
cac	gtc	atc	acc	caa	ttt	ttc	ttt	gac	gta	gaa	cgc	tac	ctg	cgc	ttc	576
His	Val	Ile	Thr	Gln	Phe	Phe	Phe	Asp	Val	Glu	Arg	Tyr	Leu	Arg	Phe	
			180					185					190			
cgc	gac	cgc	tgc	gtg	atg	ttg	ggt	atc	gat	gtg	gaa	atc	gtc	cct	ggt	624
Arg	Asp	Arg	Cys	Val	Met	Leu	Gly	Ile	Asp	Val	Glu	Ile	Val	Pro	Gly	
		195					200					205				
att	ttg	cct	gtt	acc	aac	ttc	aag	cag	ctc	ggc	aaa	atg	gcg	caa	gta	672
Ile	Leu	Pro	Val	Thr	Asn	Phe	Lys	Gln	Leu	Gly	Lys	Met	Ala	Gln	Val	
	210					215					220					
acc	aac	gtc	aaa	atc	cca	agc	tgg	ctg	tcg	caa	atg	tat	gaa	ggt	ttg	720
Thr	Asn	Val	Lys	Ile	Pro	Ser	Trp	Leu	Ser	Gln	Met	Tyr	Glu	Gly	Leu	
225					230					235					240	
gac	gac	gac	caa	ggc	acg	cgc	aac	ctc	gtc	gcc	gcc	agt	atc	gcc	atc	768
Asp	Asp	Asp	Gln	Gly	Thr	Arg	Asn	Leu	Val	Ala	Ala	Ser	Ile	Ala	Ile	
			245						250					255		
gat	atg	gtc	aaa	gtc	ctg	tcc	cgc	gaa	ggc	gtg	aaa	gat	ttc	cac	ttc	816
Asp	Met	Val	Lys	Val	Leu	Ser	Arg	Glu	Gly	Val	Lys	Asp	Phe	His	Phe	

260							265				270					
tac	acg	ctc	aac	cgc	agc	gag	ctg	act	tac	gcc	atc	tgc	cat	att	tta	864
Tyr	Thr	Leu	Asn	Arg	Ser	Glu	Leu	Thr	Tyr	Ala	Ile	Cys	His	Ile	Leu	
		275					280					285				

ggc gtg cgc cct taa 879
Gly Val Arg Pro
290

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<210> 46
<211> 292
<212> PRT
<213> Neisseria meningitidis ser. A
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Met Asn Tyr Ala Lys Glu Ile Asn Ala Leu Asn Asn Ser Leu Ser Asp  
      1              5              10             15
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Leu Lys Gly Asp Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn
20 25 30

Glu Gln Met Glu Thr Met Leu Trp Asp Ser Ile His Arg Leu Gln Thr
35 40 45

Leu His Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu
50 55 60

Arg Asp Arg Thr His Gly Ile Val Lys Arg Ile Lys Gln Glu Thr Gly
65 70 75 80

Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Ser Pro Asp Glu
85 90 95

Leu Arg Gln Ile Ala Lys Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile
100 105 110

Val Ala Leu Arg Gly Asp Glu Pro Pro Gly Tyr Glu Lys Lys Pro Phe
115 120 125

Tyr Ala Glu Asp Leu Val Lys Leu Leu Arg Ser Val Ala Asp Phe Asp
130 135 140

Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala
145 150 155 160

Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn
165 170 175

His Val Ile Thr Gln Phe Phe Phe Asp Val Glu Arg Tyr Leu Arg Phe
180 185 190

Arg Asp Arg Cys Val Met Leu Gly Ile Asp Val Glu Ile Val Pro Gly
195 200 205

Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gly Lys Met Ala Gln Val
210 215 220

Thr Asn Val Lys Ile Pro Ser Trp Leu Ser Gln Met Tyr Glu Gly Leu
225 230 235 240

Asp Asp Asp Gln Gly Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Ile
 245 250 255

Asp Met Val Lys Val Leu Ser Arg Glu Gly Val Lys Asp Phe His Phe
 260 265 270

Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Ile Leu
 275 280 285

Gly Val Arg Pro
 290

<210> 47
 <211> 849
 <212> DNA
 <213> Campylobacter jejuni

<220>
 <221> CDS
 <222> (1)..(846)
 <223> RCJ02911

<400> 47
 atg tgt agt ttt tct ttt gaa gtt ttt cca cca aga aag gat gaa aat 48
 Met Cys Ser Phe Ser Phe Glu Val Phe Pro Pro Arg Lys Asp Glu Asn
 1 5 10 15

atc aaa aat ctt cat gct atc tta gat gat tta ggg caa tta agc cct 96
 Ile Lys Asn Leu His Ala Ile Leu Asp Asp Leu Gly Gln Leu Ser Pro
 20 25 30

aat ttt atc agc gta acc ttt gga gct gga ggc tct att aac tca caa 144
 Asn Phe Ile Ser Val Thr Phe Gly Ala Gly Gly Ser Ile Asn Ser Gln
 35 40 45

aat act tta gaa gtt gca agc tta atc cag gaa gaa tat caa att cct 192
 Asn Thr Leu Glu Val Ala Ser Leu Ile Gln Glu Glu Tyr Gln Ile Pro
 50 55 60

agc ata gta cat tta cct tgc atc cat tct agt aaa gaa aaa atc act 240
 Ser Ile Val His Leu Pro Cys Ile His Ser Ser Lys Glu Lys Ile Thr
 65 70 75 80

cag ata ctt caa aaa tgc aaa gaa aaa aat ctt aat caa att ctt gcc 288
 Gln Ile Leu Gln Lys Cys Lys Glu Lys Asn Leu Asn Gln Ile Leu Ala
 85 90 95

cta aga ggc gat ata tgt gaa aat tta aaa aaa agc aaa gat ttt tct 336
 Leu Arg Gly Asp Ile Cys Glu Asn Leu Lys Lys Ser Lys Asp Phe Ser
 100 105 110

tat gct agt gat tta att tct ttt ata aaa aaa caa gaa tac ttt gaa 384
 Tyr Ala Ser Asp Leu Ile Ser Phe Ile Lys Lys Gln Glu Tyr Phe Glu
 115 120 125

att tat gcc gca tgc tat ccc gaa aaa cat aat gaa tct aaa aat ttc 432
 Ile Tyr Ala Ala Cys Tyr Pro Glu Lys His Asn Glu Ser Lys Asn Phe
 130 135 140

atc gag gat ata cac cat ctt aaa act aag gta aat gca gga aca gat 480
 Ile Glu Asp Ile His His Leu Lys Thr Lys Val Asn Ala Gly Thr Asp
 145 150 155 160
 aag ctc att act caa ctt ttt tac gat aat gaa gat ttt tat act ttt 528
 Lys Leu Ile Thr Gln Leu Phe Tyr Asp Asn Glu Asp Phe Tyr Thr Phe
 165 170 175
 aaa caa aat tgt gct tta gca gat att gac ata cct att tac gca ggt 576
 Lys Gln Asn Cys Ala Leu Ala Asp Ile Asp Ile Pro Ile Tyr Ala Gly
 180 185 190
 att atg cct att act aac aaa aga cag gtt tta aaa att tct caa ctt 624
 Ile Met Pro Ile Thr Asn Lys Arg Gln Val Leu Lys Ile Ser Gln Leu
 195 200 205
 tgc gga gct aaa atc cct cct aaa ttt gtt aaa att tta gaa aaa tat 672
 Cys Gly Ala Lys Ile Pro Lys Phe Val Lys Ile Leu Glu Lys Tyr
 210 215 220
 gaa aat aat act ttg gct tta gaa gat gca ggt atc gcg tat gct tgc 720
 Glu Asn Asn Thr Leu Ala Leu Glu Asp Ala Gly Ile Ala Tyr Ala Cys
 225 230 235 240
 gat caa att gtc gat tta atc aca agt ggt gta gat gga att cat ctt 768
 Asp Gln Ile Val Asp Leu Ile Thr Ser Gly Val Asp Gly Ile His Leu
 245 250 255
 tat act atg aat aaa tcc aaa gcg gct att aaa att tat gaa gct gta 816
 Tyr Thr Met Asn Lys Ser Lys Ala Ala Ile Lys Ile Tyr Glu Ala Val
 260 265 270
 aag cat ttg ctt aaa gaa gag ctt cat gct tag 849
 Lys His Leu Leu Lys Glu Glu Leu His Ala
 275 280

<210> 48
 <211> 282
 <212> PRT
 <213> Campylobacter jejuni

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 Met Cys Ser Phe Ser Phe Glu Val Phe Pro Pro Arg Lys Asp Glu Asn
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 Ile Lys Asn Leu His Ala Ile Leu Asp Asp Leu Gly Gln Leu Ser Pro
 20 25 30
 Asn Phe Ile Ser Val Thr Phe Gly Ala Gly Gly Ser Ile Asn Ser Gln
 35 40 45
 Asn Thr Leu Glu Val Ala Ser Leu Ile Gln Glu Glu Tyr Gln Ile Pro
 50 55 60
 Ser Ile Val His Leu Pro Cys Ile His Ser Ser Lys Glu Lys Ile Thr
 65 70 75 80
 Gln Ile Leu Gln Lys Cys Lys Glu Lys Asn Leu Asn Gln Ile Leu Ala
 85 90 95

Leu Arg Gly Asp Ile Cys Glu Asn Leu Lys Lys Ser Lys Asp Phe Ser
 100 105 110
 Tyr Ala Ser Asp Leu Ile Ser Phe Ile Lys Lys Gln Glu Tyr Phe Glu
 115 120 125
 Ile Tyr Ala Ala Cys Tyr Pro Glu Lys His Asn Glu Ser Lys Asn Phe
 130 135 140
 Ile Glu Asp Ile His His Leu Lys Thr Lys Val Asn Ala Gly Thr Asp
 145 150 155 160
 Lys Leu Ile Thr Gln Leu Phe Tyr Asp Asn Glu Asp Phe Tyr Thr Phe
 165 170 175
 Lys Gln Asn Cys Ala Leu Ala Asp Ile Asp Ile Pro Ile Tyr Ala Gly
 180 185 190
 Ile Met Pro Ile Thr Asn Lys Arg Gln Val Leu Lys Ile Ser Gln Leu
 195 200 205
 Cys Gly Ala Lys Ile Pro Pro Lys Phe Val Lys Ile Leu Glu Lys Tyr
 210 215 220
 Glu Asn Asn Thr Leu Ala Leu Glu Asp Ala Gly Ile Ala Tyr Ala Cys
 225 230 235 240
 Asp Gln Ile Val Asp Leu Ile Thr Ser Gly Val Asp Gly Ile His Leu
 245 250 255
 Tyr Thr Met Asn Lys Ser Lys Ala Ala Ile Lys Ile Tyr Glu Ala Val
 260 265 270
 Lys His Leu Lys Glu Glu Leu His Ala
 275 280

<210> 49
 <211> 852
 <212> DNA
 <213> Lactococcus lactis

<220>
 <221> CDS
 <222> (1)..(849)
 <223> AAK05352

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 Met Thr Ser Asn Ser Lys Ile Leu Ser Phe Glu Val Phe Pro Pro Thr
 1 5 10 15
 act caa att gga agt acc aac ttg gta aag acc ttg gat agc cta aga 96
 Thr Gln Ile Gly Ser Thr Asn Leu Val Lys Thr Leu Asp Ser Leu Arg
 20 25 30
 act ctc tcg cca gat ttt atc agt gta act tgt agt aac aat aat tat 144
 Thr Leu Ser Pro Asp Phe Ile Ser Val Thr Cys Ser Asn Asn Asn Tyr
 35 40 45

gat aat att gga gat aca act ata aag ttt gct gat tat gta aac aat	192
Asp Asn Ile Gly Asp Thr Thr Ile Lys Phe Ala Asp Tyr Val Asn Asn	
50 55 60	
aca cta gat att cca gcg gtt gct cat tta cct gcc gct tat tta gat	240
Thr Leu Asp Ile Pro Ala Val Ala His Leu Pro Ala Ala Tyr Leu Asp	
65 70 75 80	
aaa gct caa gtg atc gaa att ttg gaa cgg tta aaa gat aaa caa atc	288
Lys Ala Gln Val Ile Glu Ile Leu Glu Arg Leu Lys Asp Lys Gln Ile	
85 90 95	
aaa aaa att ctt gct tta aga ggt gat atc agc gat gaa ccg atg aaa	336
Lys Lys Ile Leu Ala Leu Arg Gly Asp Ile Ser Asp Glu Pro Met Lys	
100 105 110	
gat gat ttt aaa ttt gca agt gat ttg gtt aaa ttt atc aaa gat tat	384
Asp Asp Phe Lys Phe Ala Ser Asp Leu Val Lys Phe Ile Lys Asp Tyr	
115 120 125	
gat gat agt ttt gaa gtt tta ggt gct tgc tac ccc gat att cat ccc	432
Asp Asp Ser Phe Glu Val Leu Gly Ala Cys Tyr Pro Asp Ile His Pro	
130 135 140	
gaa tca gta aat cga gtg agt gat ttt cat tat ctg aaa gaa aaa gta	480
Glu Ser Val Asn Arg Val Ser Asp Phe His Tyr Leu Lys Glu Lys Val	
145 150 155 160	
gat gct ggt tgt gac aga tta atc acg caa cta ttt ttt gat aat gat	528
Asp Ala Gly Cys Asp Arg Leu Ile Thr Gln Leu Phe Phe Asp Asn Asp	
165 170 175	
agt ttc tat gat ttt caa gaa cga tgc gca att gct gag ata aat act	576
Ser Phe Tyr Asp Phe Gln Glu Arg Cys Ala Ile Ala Glu Ile Asn Thr	
180 185 190	
ccg ata ttc gcc gga ata atg cca gta atc aat cga aat caa att ctt	624
Pro Ile Phe Ala Gly Ile Met Pro Val Ile Asn Arg Asn Gln Ile Leu	
195 200 205	
cgt cta tta aaa aat tgt aat acg cca tta cca gca aaa ttc att aga	672
Arg Leu Leu Lys Asn Cys Asn Thr Pro Leu Pro Ala Lys Phe Ile Arg	
210 215 220	
ata ctc gaa aaa tat gaa cat aat ctt atc gct tta agg gat gct gga	720
Ile Leu Glu Lys Tyr Glu His Asn Leu Ile Ala Leu Arg Asp Ala Gly	
225 230 235 240	
att gct tac gcc atc gat caa atc gtt gat tta gta aca gag gat gtt	768
Ile Ala Tyr Ala Ile Asp Gln Ile Val Asp Leu Val Thr Glu Asp Val	
245 250 255	
gct gga att cac ctc tat acg atg aat aat gca aat acg gca cac tcc	816
Ala Gly Ile His Leu Tyr Thr Met Asn Asn Ala Asn Thr Ala His Ser	
260 265 270	
atc cat gct tca att tct tct tta ttt acc ttt tga	852
Ile His Ala Ser Ile Ser Ser Leu Phe Thr Phe	
275 280	

<210> 50
 <211> 283
 <212> PRT
 <213> *Lactococcus lactis*

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 20 25 30
 Thr Leu Ser Pro Asp Phe Ile Ser Val Thr Cys Ser Asn Asn Asn Tyr
 35 40 45
 Asp Asn Ile Gly Asp Thr Thr Ile Lys Phe Ala Asp Tyr Val Asn Asn
 50 55 60
 Thr Leu Asp Ile Pro Ala Val Ala His Leu Pro Ala Ala Tyr Leu Asp
 65 70 75 80
 Lys Ala Gln Val Ile Glu Ile Leu Glu Arg Leu Lys Asp Lys Gln Ile
 85 90 95
 Lys Lys Ile Leu Ala Leu Arg Gly Asp Ile Ser Asp Glu Pro Met Lys
 100 105 110
 Asp Asp Phe Lys Phe Ala Ser Asp Leu Val Lys Phe Ile Lys Asp Tyr
 115 120 125
 Asp Asp Ser Phe Glu Val Leu Gly Ala Cys Tyr Pro Asp Ile His Pro
 130 135 140
 Glu Ser Val Asn Arg Val Ser Asp Phe His Tyr Leu Lys Glu Lys Val
 145 150 155 160
 Asp Ala Gly Cys Asp Arg Leu Ile Thr Gln Leu Phe Phe Asp Asn Asp
 165 170 175
 Ser Phe Tyr Asp Phe Gln Glu Arg Cys Ala Ile Ala Glu Ile Asn Thr
 180 185 190
 Pro Ile Phe Ala Gly Ile Met Pro Val Ile Asn Arg Asn Gln Ile Leu
 195 200 205
 Arg Leu Leu Lys Asn Cys Asn Thr Pro Leu Pro Ala Lys Phe Ile Arg
 210 215 220
 Ile Leu Glu Lys Tyr Glu His Asn Leu Ile Ala Leu Arg Asp Ala Gly
 225 230 235 240
 Ile Ala Tyr Ala Ile Asp Gln Ile Val Asp Leu Val Thr Glu Asp Val
 245 250 255
 Ala Gly Ile His Leu Tyr Thr Met Asn Asn Ala Asn Thr Ala His Ser
 260 265 270
 Ile His Ala Ser Ile Ser Ser Leu Phe Thr Phe
 275 280

<210> 51
 <211> 891
 <212> DNA
 <213> *Prochlorococcus maritima*

<220>
 <221> CDS
 <222> (1) .. (888)
 <223> RCK01602

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 1 5 10 15

aca gca gaa tta atg ccg cca aga gga gga gac ccc gta aga tct ctt 96
 Thr Ala Glu Leu Met Pro Pro Arg Gly Gly Asp Pro Val Arg Ser Leu
 20 25 30

aaa ata gca caa ctc ttg aga aat aag gtg cat gca gtt aat att aca 144
 Lys Ile Ala Gln Leu Leu Arg Asn Lys Val His Ala Val Asn Ile Thr
 35 40 45

gac gga agt aga gca ata atg aga atg tgt agt tta gca atg tct aaa 192
 Asp Gly Ser Arg Ala Ile Met Arg Met Cys Ser Leu Ala Met Ser Lys
 50 55 60

cta tta cta gac aat ggg ata gaa cct ata atg cag atc tca tgt aga 240
 Leu Leu Leu Asp Asn Gly Ile Glu Pro Ile Met Gln Ile Ser Cys Arg
 65 70 75 80

gat cgt aat aaa att gct tta caa tca gat att ctt gga gca aat gcc 288
 Asp Arg Asn Lys Ile Ala Leu Gln Ser Asp Ile Leu Gly Ala Asn Ala
 85 90 95

tta gga att aaa aat att tta tgc att aca gga gat tct gta aaa gcc 336
 Leu Gly Ile Lys Asn Ile Leu Cys Ile Thr Gly Asp Ser Val Lys Ala
 100 105 110

gga gat cag caa gaa aca aaa gcc gtt cat gaa ttt gag gca gta aga 384
 Gly Asp Gln Gln Glu Thr Lys Ala Val His Glu Phe Glu Ala Val Arg
 115 120 125

tta tta aaa caa att caa tca ttc aat caa gga att gat cct act ttt 432
 Leu Leu Lys Lys Gln Ile Gln Ser Phe Asn Gln Gly Ile Asp Pro Thr Phe
 130 135 140

gaa caa ctt cca gac aaa agg act gaa att ttc tca ggt gcg gca gta 480
 Glu Gln Leu Pro Asp Lys Arg Thr Glu Ile Phe Ser Gly Ala Ala Val
 145 150 155 160

gat cca agt tgt cga aat caa aga agt tta aaa agt aga aca att aaa 528
 Asp Pro Ser Cys Arg Asn Gln Arg Ser Leu Lys Ser Arg Thr Ile Lys
 165 170 175

aaa aaa gag gcc ggt gca aat ttc tta caa act caa ata gtt atg gat 576
 Lys Lys Glu Ala Gly Ala Asn Phe Leu Gln Thr Gln Ile Val Met Asp
 180 185 190

aga aaa tgt tta gca gac ttt tgc aac gaa atc agt aat cca ctt gag 624

Arg Lys Cys Leu Ala Asp Phe Cys Asn Glu Ile Ser Asn Pro Leu Glu
 195 200 205
 ata cca gtt att gca gga gta ttt ctt tta aaa tca tat aaa aat gct 672
 Ile Pro Val Ile Ala Gly Val Phe Leu Leu Lys Ser Tyr Lys Asn Ala
 210 215 220
 ctt ttc ata aat aaa ttt gta cct gga gcg aat att cct gaa aat gtt 720
 Leu Phe Ile Asn Lys Phe Val Pro Gly Ala Asn Ile Pro Glu Asn Val
 225 230 235 240
 tta aat cgt ctc aaa gat gca aaa aat cca ctt caa gaa gga ata tta 768
 Leu Asn Arg Leu Lys Asp Ala Lys Asn Pro Leu Gln Glu Gly Ile Leu
 245 250 255
 att gct tca gag caa gct caa gat ttt att aat att gca gat gga att 816
 Ile Ala Ser Glu Gln Ala Gln Asp Phe Ile Asn Ile Ala Asp Gly Ile
 260 265 270
 cat ctt atg gca gtc aaa tca gaa cat ctt atc cca gag ata ctt gaa 864
 His Leu Met Ala Val Lys Ser Glu His Leu Ile Pro Glu Ile Leu Glu
 275 280 285
 aaa gct ggt ctc aat ctg gaa tgt taa 891
 Lys Ala Gly Leu Asn Leu Glu Cys
 290 295

<210> 52
 <211> 296
 <212> PRT
 <213> Prochlorococcus maritima

<400> 52
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 Thr Ala Glu Leu Met Pro Pro Arg Gly Gly Asp Pro Val Arg Ser Leu
 20 25 30
 Lys Ile Ala Gln Leu Leu Arg Asn Lys Val His Ala Val Asn Ile Thr
 35 40 45
 Asp Gly Ser Arg Ala Ile Met Arg Met Cys Ser Leu Ala Met Ser Lys
 50 55 60
 Leu Leu Leu Asp Asn Gly Ile Glu Pro Ile Met Gln Ile Ser Cys Arg
 65 70 75 80
 Asp Arg Asn Lys Ile Ala Leu Gln Ser Asp Ile Leu Gly Ala Asn Ala
 85 90 95
 Leu Gly Ile Lys Asn Ile Leu Cys Ile Thr Gly Asp Ser Val Lys Ala
 100 105 110
 Gly Asp Gln Gln Glu Thr Lys Ala Val His Glu Phe Glu Ala Val Arg
 115 120 125
 Leu Leu Lys Gln Ile Gln Ser Phe Asn Gln Gly Ile Asp Pro Thr Phe
 130 135 140

Glu Gln Leu Pro Asp Lys Arg Thr Glu Ile Phe Ser Gly Ala Ala Val
 145 150 155 160
 Asp Pro Ser Cys Arg Asn Gln Arg Ser Leu Lys Ser Arg Thr Ile Lys
 165 170 175
 Lys Lys Glu Ala Gly Ala Asn Phe Leu Gln Thr Gln Ile Val Met Asp
 180 185 190
 Arg Lys Cys Leu Ala Asp Phe Cys Asn Glu Ile Ser Asn Pro Leu Glu
 195 200 205
 Ile Pro Val Ile Ala Gly Val Phe Leu Leu Lys Ser Tyr Lys Asn Ala
 210 215 220
 Leu Phe Ile Asn Lys Phe Val Pro Gly Ala Asn Ile Pro Glu Asn Val
 225 230 235 240
 Leu Asn Arg Leu Lys Asp Ala Lys Asn Pro Leu Gln Glu Gly Ile Leu
 245 250 255
 Ile Ala Ser Glu Gln Ala Gln Asp Phe Ile Asn Ile Ala Asp Gly Ile
 260 265 270
 His Leu Met Ala Val Lys Ser Glu His Leu Ile Pro Glu Ile Leu Glu
 275 280 285
 Lys Ala Gly Leu Asn Leu Glu Cys
 290 295

<210> 53
 <211> 1848
 <212> DNA
 <213> Bacillus stearothermophilus

<220>
 <221> CDS
 <222> (1)..(1845)
 <223> RBE04103

<400> 53
 gtg gga ttg ctg gat gag ttg aaa gag cgc att ctc atc gcc gac ggg 48
 Val Gly Leu Leu Asp Glu Leu Lys Glu Arg Ile Leu Ile Ala Asp Gly
 1 5 10 15
 gcg atg gga acg ctt tta tat tcg cac ggc att gac cgt tgt ttt gaa 96
 Ala Met Gly Thr Leu Leu Tyr Ser His Gly Ile Asp Arg Cys Phe Glu
 20 25 30
 gaa ttg aat cta tcc aat cca gat gaa atc gtc cat att cat gaa gcg 144
 Glu Leu Asn Leu Ser Asn Pro Asp Glu Ile Val His Ile His Glu Ala
 35 40 45
 tat atc gcc gcg ggc gcc gac gtc att cag acg aat aca tac ggc gcc 192
 Tyr Ile Ala Ala Gly Ala Asp Val Ile Gln Thr Asn Thr Tyr Gly Ala
 50 55 60
 aac tat gtg aaa ctc gcc cgc tac ggc ctt gaa gat gag gtg ccg gcc 240
 Asn Tyr Val Lys Leu Ala Arg Tyr Gly Leu Glu Asp Glu Val Pro Ala

65	70	75	80	
atc aac cgc gcg gcg gtg cgg ctc gcc agg caa gcg gcg aac gga cgg				288
Ile Asn Arg Ala Ala Val Arg Leu Ala Arg Gln Ala Ala Asn Gly Arg	85	90	95	
gca tac gtg ctc ggg acg atc ggg ggg ctg cgc acg tta aac aaa agc				336
Ala Tyr Val Leu Gly Thr Ile Gly Gly Leu Arg Thr Leu Asn Lys Ser	100	105	110	
gtc gtc acg ctc gaa gaa gtg aag cgg acg ttt cgc gag cag ctg ttt				384
Val Val Thr Leu Glu Glu Val Lys Arg Thr Phe Arg Glu Gln Leu Phe	115	120	125	
gtc ctg ctc gct gaa ggg gtc gac ggc gtg ctg ctc gag acg tat tac				432
Val Leu Leu Ala Glu Gly Val Asp Gly Val Leu Leu Glu Thr Tyr Tyr	130	135	140	
gat ttg gaa gag ttg gag acg gtg ctt gcc atc gcc cgc aaa gag acc				480
Asp Leu Glu Glu Leu Glu Thr Val Leu Ala Ile Ala Arg Lys Glu Thr	145	150	155	160
gac ttg ccg att atc gct cac gtc tcg ctc cat gaa gtc ggc gtc ttg				528
Asp Leu Pro Ile Ile Ala His Val Ser Leu His Glu Val Gly Val Leu	165	170	175	
caa gat ggc acg ccg ctc gcg gac gcc ctt gcc cgc cta gag gcg ctc				576
Gln Asp Gly Thr Pro Leu Ala Asp Ala Leu Ala Arg Leu Glu Ala Leu	180	185	190	
ggg gcc gat gtc gtc gga ctg aac tgt cgt ctc ggt cca tat cat atg				624
Gly Ala Asp Val Val Gly Leu Asn Cys Arg Leu Gly Pro Tyr His Met	195	200	205	
ctt cgg tcg ctc gag gaa gtg ccg ctg cca aat cga gcg ttt ttg tcg				672
Leu Arg Ser Leu Glu Glu Val Pro Leu Pro Asn Arg Ala Phe Leu Ser	210	215	220	
gcg tat ccg aac gcc agc ctt ccg gat tac cgc gat ggg cgg ctt gtc				720
Ala Tyr Pro Asn Ala Ser Leu Pro Asp Tyr Arg Asp Gly Arg Leu Val	225	230	235	240
tat gag acg aac gct gaa tat ttc gag gaa acg gcc aaa gcg ttc cgc				768
Tyr Glu Thr Asn Ala Glu Tyr Phe Glu Glu Thr Ala Lys Ala Phe Arg	245	250	255	
gac caa ggg gtg cgc ttg atc ggc ggg tgc tgc ggc acg acg ccg aaa				816
Asp Gln Gly Val Arg Leu Ile Gly Gly Cys Cys Gly Thr Thr Pro Lys	260	265	270	
cat atc gaa gcg atg gca aaa gcg ctc tcc gac cga acg ccg gtg acg				864
His Ile Glu Ala Met Ala Lys Ala Leu Ser Asp Arg Thr Pro Val Thr	275	280	285	
gaa aaa acg gtg aaa cgg cgc gcg gtg tct gta tca gtg caa gcg gag				912
Glu Lys Thr Val Lys Arg Arg Ala Val Ser Val Ser Val Gln Ala Glu	290	295	300	
cgg ccc gcc cca tct ccc ctt ccc gag ctt gcc cgc acg cac cgc tcg				960
Arg Pro Ala Pro Ser Pro Leu Pro Glu Leu Ala Arg Thr His Arg Ser	305	310	315	320

gtc att gtg gag ctg gat ccg ccg aaa aaa ttg ggg att gac aag ttt	1008
Val Ile Val Glu Leu Asp Pro Pro Lys Lys Leu Gly Ile Asp Lys Phe	
325 330 335	
ctt gcc ggg gcg aaa gcg ctc cat gac gcc ggc atc gat gcg ctg acg	1056
Leu Ala Gly Ala Lys Ala Leu His Asp Ala Gly Ile Asp Ala Leu Thr	
340 345 350	
ttg gcc gac aac tcg ctc gcc acg ccg cgc atc agc aac gcc gct gtc	1104
Leu Ala Asp Asn Ser Leu Ala Thr Pro Arg Ile Ser Asn Ala Ala Val	
355 360 365	
gcc acg atc atc aag gag caa ctc ggc atc cgc ccg ctc gtg cat att	1152
Ala Thr Ile Ile Lys Glu Gln Leu Gly Ile Arg Pro Leu Val His Ile	
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aca tgc cgc gat cgc aat ttg atc ggc ttg cag tcg cat ttg atg ggc	1200
Thr Cys Arg Asp Arg Asn Leu Ile Gly Leu Gln Ser His Leu Met Gly	
385 390 395 400	
ttg cat acg ctc ggc atc acc gat gtg ctc gcc att acc ggc gac ccg	1248
Leu His Thr Leu Gly Ile Thr Asp Val Leu Ala Ile Thr Gly Asp Pro	
405 410 415	
tcg aaa atc ggc gat ttt cca ggg gca acg tcc gtg tac gac tta tca	1296
Ser Lys Ile Gly Asp Phe Pro Gly Ala Thr Ser Val Tyr Asp Leu Ser	
420 425 430	
tcg ttc gat ttg atc cgc ttg atc cgc cag ttt aac gaa ggg ctg tcg	1344
Ser Phe Asp Leu Ile Arg Leu Ile Arg Gln Phe Asn Glu Gly Leu Ser	
435 440 445	
tac tcg ggc aaa ccg ctt ggg caa aaa acg aac ttc tcg atc ggc gct	1392
Tyr Ser Gly Lys Pro Leu Gly Gln Lys Thr Asn Phe Ser Ile Gly Ala	
450 455 460	
gcg ttc aac ccg aac gtc cgc cat ttg gac aaa gcg gtc gag cgg atg	1440
Ala Phe Asn Pro Asn Val Arg His Leu Asp Lys Ala Val Glu Arg Met	
465 470 475 480	
gag aaa aaa atc caa tgc ggc gcc cat tat ttc ttg acc cag ccg att	1488
Glu Lys Lys Ile Gln Cys Gly Ala His Tyr Phe Leu Thr Gln Pro Ile	
485 490 495	
tac tcg gaa gag aaa atc gtt gaa gtg cac gaa gcg acc aag cat ctt	1536
Tyr Ser Glu Glu Lys Ile Val Glu Val His Glu Ala Thr Lys His Leu	
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gac acg ccg att tac atc ggc att atg ccg ctt gtg agc gcg cgc aac	1584
Asp Thr Pro Ile Tyr Ile Gly Ile Met Pro Leu Val Ser Ala Arg Asn	
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gcc gac ttt ttg cat cat gaa gtg ccg ggc att acg ctc tct gac gag	1632
Ala Asp Phe Leu His His Glu Val Pro Gly Ile Thr Leu Ser Asp Glu	
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Ile Arg Ala Arg Met Ala Ala Cys Ser Gly Asp Pro Val Gln Ala Ala	
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aag gaa ggc atc gct atc gcc aaa tcg ctc att gac gct gcg ttt gat 1728
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 565 570 575

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 610 615

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 Tyr Ile Ala Ala Gly Ala Asp Val Ile Gln Thr Asn Thr Tyr Gly Ala
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 Asn Tyr Val Lys Leu Ala Arg Tyr Gly Leu Glu Asp Glu Val Pro Ala
 65 70 75 80

 Ile Asn Arg Ala Ala Val Arg Leu Ala Arg Gln Ala Ala Asn Gly Arg
 85 90 95

 Ala Tyr Val Leu Gly Thr Ile Gly Gly Leu Arg Thr Leu Asn Lys Ser
 100 105 110

 Val Val Thr Leu Glu Glu Val Lys Arg Thr Phe Arg Glu Gln Leu Phe
 115 120 125

 Val Leu Leu Ala Glu Gly Val Asp Gly Val Leu Leu Glu Thr Tyr Tyr
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 Asp Leu Glu Glu Leu Glu Thr Val Leu Ala Ile Ala Arg Lys Glu Thr
 145 150 155 160

 Asp Leu Pro Ile Ile Ala His Val Ser Leu His Glu Val Gly Val Leu
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 Gln Asp Gly Thr Pro Leu Ala Asp Ala Leu Ala Arg Leu Glu Ala Leu
 180 185 190

 Gly Ala Asp Val Val Gly Leu Asn Cys Arg Leu Gly Pro Tyr His Met

195	200	205
Leu Arg Ser Leu Glu Glu Val 210	Pro Leu Pro Asn Arg Ala Phe Leu Ser 215	
Ala Tyr Pro Asn Ala Ser Leu Pro Asp Tyr Arg Asp Gly Arg Leu Val 225		235 240
Tyr Glu Thr Asn Ala Glu Tyr Phe Glu Glu Thr Ala Lys Ala Phe Arg 245	250	255
Asp Gln Gly Val Arg Leu Ile Gly Gly Cys Cys Gly Thr Thr Pro Lys 260	265	270
His Ile Glu Ala Met Ala Lys Ala Leu Ser Asp Arg Thr Pro Val Thr 275	280	285
Glu Lys Thr Val Lys Arg Arg Ala Val Ser Val Ser Val Gln Ala Glu 290	295	300
Arg Pro Ala Pro Ser Pro Leu Pro Glu Leu Ala Arg Thr His Arg Ser 305	310	315 320
Val Ile Val Glu Leu Asp Pro Pro Lys Lys Leu Gly Ile Asp Lys Phe 325	330	335
Leu Ala Gly Ala Lys Ala Leu His Asp Ala Gly Ile Asp Ala Leu Thr 340	345	350
Leu Ala Asp Asn Ser Leu Ala Thr Pro Arg Ile Ser Asn Ala Ala Val 355	360	365
Ala Thr Ile Ile Lys Glu Gln Leu Gly Ile Arg Pro Leu Val His Ile 370	375	380
Thr Cys Arg Asp Arg Asn Leu Ile Gly Leu Gln Ser His Leu Met Gly 385	390	395 400
Leu His Thr Leu Gly Ile Thr Asp Val Leu Ala Ile Thr Gly Asp Pro 405	410	415
Ser Lys Ile Gly Asp Phe Pro Gly Ala Thr Ser Val Tyr Asp Leu Ser 420	425	430
Ser Phe Asp Leu Ile Arg Leu Ile Arg Gln Phe Asn Glu Gly Leu Ser 435	440	445
Tyr Ser Gly Lys Pro Leu Gly Gln Lys Thr Asn Phe Ser Ile Gly Ala 450	455	460
Ala Phe Asn Pro Asn Val Arg His Leu Asp Lys Ala Val Glu Arg Met 465	470	475 480
Glu Lys Lys Ile Gln Cys Gly Ala His Tyr Phe Leu Thr Gln Pro Ile 485	490	495
Tyr Ser Glu Glu Lys Ile Val Glu Val His Glu Ala Thr Lys His Leu 500	505	510
Asp Thr Pro Ile Tyr Ile Gly Ile Met Pro Leu Val Ser Ala Arg Asn 515	520	525

Ala Asp Phe Leu His His Glu Val Pro Gly Ile Thr Leu Ser Asp Glu
 530 535 540

Ile Arg Ala Arg Met Ala Ala Cys Ser Gly Asp Pro Val Gln Ala Ala
 545 550 555 560

Lys Glu Gly Ile Ala Ile Ala Lys Ser Leu Ile Asp Ala Ala Phe Asp
 565 570 575

Leu Phe Asn Gly Ile Tyr Leu Ile Thr Pro Phe Leu Arg Tyr Asp Met
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Thr Val Glu Leu Val Arg Tyr Ile His Glu Lys Glu Ala Ala Ala Lys
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Glu Arg Lys Val Val His Gly
 610 615

<210> 55

<211> 52

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

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<210> 56

<211> 53

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 56

tctagactcg agcggccgcg gccggccttt aaattgaaga cgaaagggcc tcg 53

<210> 57

<211> 47

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence:PCR primer

<400> 57

gagatctaga cccgggggatc cgctagcggg ctgctaaagg aagcgga 47

<210> 58

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 58

gagagggcgcg ccgctagcgt gggcgaagaa ctccagca

38

<210> 59

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

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34

<210> 60

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

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34

<210> 61

<211> 140

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 61

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<210> 62

<211> 140

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence:PCR primer

<400> 62

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 aggcctctcg agatttaaatt 140

<210> 63

<211> 33

<212> DNA
 <213> Artificial sequence

<220>

<223> Description of the artificial sequence:PCR primer

<400> 63

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33

<210> 64

<211> 32

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence:PCR primer

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32

<210> 65

<211> 5091

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence:plasmid

<400> 65

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<210> 66

<211> 4323

<212> DNA

<213> Artificial sequence

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<223> Description of the artificial sequence: plasmid

<400> 66

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<210> 67

<211> 35

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR Primer

<400> 67

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35

<210> 68

<211> 34

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR Primer

<400> 68

ctctctctgt cgacgaattc aatcttacgg cctg

34

<210> 69

<211> 5860

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmid

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<210> 70

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR Primer

<400> 70

cggcaccacc gacatcatct tcacctgcc tcgttccg

38

<210> 71

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: PCR Primer

<400> 71

cggaacgagg gcagggtgaag atgatgtcgg tggtgccg

38

<210> 72

<211> 1266

<212> DNA

<213> LysC mutant

<220>

<221> CDS

<222> (1)..(1266)

<223>

<400> 72

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gaa cgc att aga aac gtc gct gaa cgg atc gtt gcc acc aag aag gct	96
Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala	
20 25 30	

gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat	144
Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp	
35 40 45	

gaa ctt cta gaa ctt gca gcg gca gtg aat ccc gtt ccg cca gct cgt	192
Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg	
50 55 60	

gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc	240
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu	
65 70 75 80	

gtc gcc atg gct att gag tcc ctt ggc gca gaa gcc caa tct ttc acg	288
Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr	
85 90 95	

ggc tct cag gct ggt gtg ctc acc acc gag cgc cac gga aac gca cgc	336
Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg	
100 105 110	

att gtt gat gtc act cca ggt cgt gtg cgt gaa gca ctc gat gag ggc	384
Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly	
115 120 125	

aag atc tgc att gtt gct ggt ttc cag ggt gtt aat aaa gaa acc cgc	432
Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg	
130 135 140	

gat gtc acc acg ttg ggt cgt ggt ggt tct gac acc act gca gtt gcg	480
Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala	
145 150 155 160	

ttg gca gct gct ttg aac gct gat gtg tgt gag att tac tcg gac gtt	528
Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val	

165	170	175	
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gca ggc acc gga cgc taa
 Ala Gly Thr Gly Arg
 420

1266

<210> 73

<211> 421

<212> PRT

<213> LysC mutant

<400> 73

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Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
 35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
 50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
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Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
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Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
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Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
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Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
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Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
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Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
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Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
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Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
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Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
 260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
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Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
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Asp Gly Thr Thr Asp Ile Ile Phe Thr Cys Pro Arg Ser Asp Gly Arg
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Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
 325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
 340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
 355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
 370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
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Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
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Ala Gly Thr Gly Arg
420

<210> 74

<211> 5860

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: plasmid

<400> 74

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